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**THIS PAGE BLANK (USPTO)**

92044

From: Gibbs, Terra  
 Sent: Tuesday, April 22, 2003 10:53 AM  
 To: STIC-Biotech/ChemLib  
 Subject: Sequence search request...

P

Could you please do a regular search of SEQ ID NO:3 of USSN 09/918026?

Terra Gibbs #79523  
 AU 1635  
 Mailbox 11E12  
 306-3221

THANK YOU!

Point of Contact:  
 Beverly Shears  
 Technical Info. Specialist  
 M1 1E05 Tel: 308-4994

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: \_\_\_\_\_  
 Date Completed: \_\_\_\_\_  
 Searcher Prep/Review: \_\_\_\_\_  
 Clerical: \_\_\_\_\_  
 Online time: \_\_\_\_\_

TYPE OF SEARCH:  
 NA Sequences: \_\_\_\_\_  
 AA Sequences: \_\_\_\_\_  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 03:25:07 ; Search time 2934 Seconds  
(without alignments)  
15563.157 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggagccggcgccggccg.....cttggtcctgccatacctag 1569

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_hgt:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pi:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pi:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
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- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_man:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1569	100.0	1569	9	AF099031	Homo sapi
2	1564.2	99.7	2040	9	AF059203	Homo sapi
3	1459	93.0	2078	9	AF053234	Chloroce
4	1129.6	72.0	1933	10	AB075946	Rattus no
5	1115	71.1	2170	10	BC025931	Mus muscu
6	1112.4	70.9	1607	10	AF078751	Mus muscu
7	421.4	26.9	3041	10	S81092	acyl-coenzy
8	421.4	26.9	3697	10	MUSACT	Mus muscu
9	412.2	26.3	1750	10	D86373	Rattus norv
10	410.4	26.2	1673	9	AF053336	Chloroce
11	407.2	26.0	4011	9	HUMACYLCOA	Homo sapien
12	406.4	25.9	3024	10	CGU47320	Cricketul
13	405.8	25.9	1528	9	AF354622	Gorilla g
14	405.6	25.9	3407	9	BC028940	Homo sapi
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16	405.6	25.9	4011	6	AR080271	Sequence
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18	404	25.7	1672	9	AF053337	Macaca fa
19	404	25.7	1672	9	AK026611	Homo sapi
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21	402.8	25.7	1528	9	AF354623	Pongo pyg
22	359.8	22.9	4079	6	AR053911	Sequence
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28	268.2	17.1	157807	9	AC073573	Homo sapi
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31	173.8	11.1	163811	2	AC110347	Rattus no
32	172	11.0	74310	2	AC013041	Drosophi
33	172	11.0	167467	3	AC009512	Drosophi
34	172	11.0	186322	3	AC008314	Drosophi
35	172	11.0	242566	3	AE003680	Drosophi
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38	150.4	9.6	176	9	F331502S14	Homo sapi
39	142.6	9.1	181870	2	AC024216	Homo sapi
40	140.4	8.9	177	9	F331502S03	Homo sapi
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ALIGNMENTS

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LOCUS

DEFINITION

complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF099031 1569 bp mRNA linear PRI 11-SEP-2000  
Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA,  
complete cds.

AF099031 GI:4878036

Homo sapiens.

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1569)

Chang,C.C., Sakashita,N., Ornvold,K., Lee,O., Chang,E.T., Dong,R.,

Lin,S., Lee,C.Y., Strom,S.C., Kashyap,R., Fung,J.J., Farese,R.V.

Jr., Patoiseau, J.F., Delhon, A. and Chang, T.Y.,  
Immunological quantitation and localization of ACAT-1 and ACAT-2 in  
human liver and small intestine  
J. Biol. Chem. 275 (36), 28083-28092 (2000)  
20428724  
PUBMED  
10846185  
REFERENCE  
2 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Human ACAT-2 nucleotide sequence  
Unpublished  
JOURNAL  
3 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Direct Submission  
Submitted (15-OCT-1998) Biochemistry, Dartmouth, HB 7200, Hanover,  
NH 03755, USA  
REFERENCE  
4 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Direct Submission  
Submitted (20-MAY-1999) Biochemistry, Dartmouth, HB 7200, Hanover,  
NH 03755, USA  
REMARK  
Sequence update by submitter  
COMMENT  
On May 20, 1999 this sequence version replaced gi:3892234.  
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source

gene

CDS

BASE COUNT  
ORIGIN

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RESULT 3
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mRNA, complete cds.
ACCESSION
AF053234.1
VERSION
AF053234.1
KEYWORDS
GI:3582751
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ORGANISM
Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
1 (bases 1 to 2078)
Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M.,
Shelness, G.S. and Rudel, L.L.
Identification of a form of acyl-CoA:cholesterol acyltransferase
specific to liver and intestine in nonhuman primates
J. Biol. Chem. 273 (41), 26747-26754 (1998)
98434590
PUBMED
9756918
REFERENCE
2 (bases 1 to 2078)
Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M.,
Shelness, G. and Rudel, L.L.
Direct Submission
Submitted (10-MAR-1998) Internal Medicine, Wake Forest University
School of Medicine, Medical Center Boulevard, Winston-Salem, NC
27157, USA
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LOCUS AF078751  
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ACCESSION AF078751  
VERSION AF078751.1 GI:3746693  
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SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
REFERENCE 1 (bases 1 to 1607)  
AUTHORS Cases, S., Novak, S., Zheng, Y. W., Myers, H. M., Lear, S. R., Sande, E.,  
Welch, C. B., Luis, A. J., Spencer, T. A., Krause, B. R., Erickson, S. K.  
and Faresse, R. V. Jr.  
TITLE ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase.  
J. Biol. Chem. 273 (41), 26755-26764 (1998)  
MEDLINE 98434591  
PUBMED 9756919  
REFERENCE 2 (bases 1 to 1607)  
AUTHORS Faresse, R. V. Jr.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-1998) Gladstone Institute, 2550 23rd Street, San  
Francisco, CA 94110, USA  
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QY	1480 TTCTAGGTTTTTGTGCCAACATACGTTGTCTTTAGCATACACTGCCACGACGCTCCCGGT 1539				
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**source**

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Best Local Similarity 58.7%; Pred. NO. 2.6e-72;  
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RESULT 10

REF ID: A6053336

LOCUS

### DEFINITION

ACCESSION

VERSION  
KEYWORDS

**KEYWORDS**  
**SOURCE**

DOORCE  
ORGANISMS

.....

## REFERENCE

## AUTHORS

TTTTT

### 3711

JOURNAL.

MEDLINE

PUBMED

## REFERENCE

## AUTHORS

AF053336 1673 bp mRNA linear PRI 12-JUL-1993  
Chlorocebus aethiops acyl-CoA:cholesterol acyltransferase 1 (ACAT1)  
mRNA, complete cds.  
AF053336  
AF053336.1 GI:3582756  
Cercopithecus aethiops.  
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
Cercopithecinae; Cercopithecus.  
1 (bases 1 to 1673)  
Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M.,  
Shelness, G.S. and Rudel, L.L.  
Identification of a form of acyl-CoA:cholesterol acyltransferase  
specific to liver and intestine in nonhuman primates  
J. Biol. Chem. 273 (41), 26747-26754 (1998)  
98434590  
9756918  
2 (bases 1 to 1673)  
Anderson, R.A., Joyce, C., Davis, M., Reagan, J., Clark, M., Shelness, G.  
and Rudel, L.L.



TITLE Direct Submission  
JOURNAL Submitted (11-MAR-1998) Internal Medicine, Wake Forest University  
School of Medicine, Medical Center Boulevard, Winston-Salem, NC  
27157, USA

## FEATURES

## source

Location/Qualifiers

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1. .1653

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Best Local Similarity 59.1%; Pred. No. 6e-72;

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## RESULT 11

## HUMACYLCOA

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

4011 bp mRNA linear PRI 20-MAY-1999  
Homo sapiens acyl-coenzyme A: cholesterol acyltransferase mRNA,  
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L21934  
L21934.2 GI:4878021  
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Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 4011)  
Chang,C.C., Huh,H.Y., Cadigan,K.M. and Chang,T.Y.  
Molecular cloning and functional expression of human acyl-coenzyme  
A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary  
cells  
J. Biol. Chem. 268 (28), 20747-20755 (1993)  
94012607





REFERENCE 1 (bases 1 to 3024)  
 AUTHORS Cao, G., Goldstein, J.L. and Brown, M.S.  
 TITLE Complementation of mutation in acyl-CoA:cholesterol acyltransferase (ACAT) fails to restore sterol regulation in ACAT-defective sterol-resistant hamster cells  
 J. Biol. Chem. 271 (24), 14642-14648 (1996)  
 MEDLINE 96278939  
 PUBMED 8662991  
 REFERENCE 2 (bases 1 to 3024)  
 AUTHORS Cao, G., Brown, M.S. and Goldstein, J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-1996) Guoqing Cao, Molecular Genetics, University of Texas Southwestern, 5323 Harry Hines Blvd., Dallas, TX 75235, USA

## FEATURES

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AF354622

LOCUS

DEFINITION

AF354622

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF354622 1528 bp mRNA linear PRI 17-APR-2002  
 Gorilla gorilla cholesterol acyltransferase 1 (ACAT1) mRNA, partial cds.  
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 Gorilla gorilla.  
 Gorilla gorilla.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 1 (bases 1 to 1528)  
 Stauffer, R.L., Walker, A., Ryder, O.A., Lyons-Weiler, M. and





RESULT 15  
LOCUS AR053912 4011 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5834283.  
ACCESSION AR053912  
VERSION AR053912.1 GI:5978774  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4011)  
AUTHORS Chang, F.-Y. and Chang, C.C.-Y.  
TITLE Acyl coenzyme A:cholesterol acyltransferase (ACAT)  
JOURNAL Patent: US 5834283-A 3 10-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..4011  
BASE COUNT 1056 a 792 c 839 g 1324 t  
ORIGIN  
Query Match 25.98; Score 405.6; DB 6; Length 4011;  
Best Local Similarity 58.98; Pred. No. 5e-71;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3:  
Qy 287 CATCCCTGGGAAACAGAAAGCTTTTCATCCGCAAGTCCCTGCTTGATGAGCTGATGG 346  
Db 1737 CACCTCCAGAACAGAAAGATTTTATTGCAAGCGCTCTCTAGATGAACCTGCTG 1796.  
Qy 347 AGGTGACGATTTCCGACCACTATACACATGTTTATCGCTGGGCTGTGTCTTCATCA 406  
Db 1797 AAGTGGACCACTAGAACAAATATACATGTTTATTGCGCTCTCTATCTCTTTATCC 1856  
Qy 407 TCAGCACCTCGCCATCGACTTCATGATGAGGCGAGCTCTGCTGGAGTTTGACCTAC 466  
Db 1857 TCAGCACACTGTAGTATTACATGATGAAGGAAGCTGGTCTGAGTTCAGCTCC 1916  
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTCTGT 526  
Db 1917 TGTCTATGCTTTTGGCAAAATTTCTACCGTGTGTTGGACCTGGTGGATCATGTTCTGT 1976  
Qy 527 CCACCTGTTGGCGCGTACAGGCGCTTACGCGTGTGGGCGAGGGGACCTGGAGCGAGG 586  
Db 1977 CTACATTTTCAAGTTCCCTATTTCTGTTTCAACATATTGGCGACTGGCTATAGCAAGAGT 2036  
Qy 587 CGACGGGCTCGGCTGTGCGCTTTTAGCGCCACCGCTGGTGTCTGCGCGCTGCGCGG 646  
Db 2037 CTCATCCGCTGATCGGTCTCTTCCATGGCTTTCTTTTCATGATCTTCAGATTGGAG 2096  
Qy 647 TCC-----ACGTGGCCGTGGAGCATCAGCTCCCGCGGCGCTCCCGTT 688  
Db 2097 TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACGCTTCCCGGT 2156  
Qy 689 GTGTCCTGGCTTCGACGAGGTAGTTCCTGATGAAGACTACTCTTCTCTGAGAGAGG 748  
Db 2157 TCATCATATATTCGAGCAGATTCGTTTGTAAATGAAGGCCCACTCAATTTGTCAGAGAGA 2216  
Qy 749 CTGTGCTGGGATCCTTCGTCGCCACGAGGTGAGGGATCCAGGCCCCCAGTTTCTCCA 808  
Db 2217 ACGTGCTCGGGTACTAAAT--TCAGCTAAGGAGAAATCAAGCACTGTTTCCAATACCTACA 2275  
Qy 809 G-----CTACCTCTACTTCTCTTCTGCGCCAACTATCTACAGGGAGACTTACCC 861  
Db 2276 GTCACACAGTATTGTACTTCTTATTTGCTCTTACCTTATCTACCGTGACAGCTATCCC 2335  
Qy 862 AGGACGCCCTATGTCAGGTGGAATATGTGGCCAAGAACTTTGCCAGGCCCTGGGATGT 921  
Db 2336 AGGAATCCCACTGTAAGATGGGTTATGTCGCTATGAAGTTTGCACAGGTCTTTGGTTGC 2395  
Qy 922 GTGCTCTATGCTGCTTCATCCTCGGGCGGCTGTGTGTTCTGTCTTTGCCAATGAGC 981  
Db 2396 TTTTCTATGTGTACTACATCTTTGAAAGGCTTTGTGCCCTTGTTCGGAATATCAA 2455

Qy 982 CGAGAGCCCTTCAGCACCCGTCCTGCTGCTCTATCTCCATGCCACGCTTGCCAGGC 1041  
Db 2456 CAGGAGCCCTTCAGGCTCGTCTGCTCTATGCTATTTAACTCATCTTGCAGGT 2515  
Qy 1042 ATCTTCATGCTGCTGCTCATCTTCTTCCCTTCCTCCATGCTGCTCAAGCCCTTGC 1101  
Db 2516 GTGCTGATTCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2575  
Qy 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGACTGGTGAACCTCAACGCTTTC 1161  
Db 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTCATGAACCTCAACGCTATAC 2635  
Qy 1162 TCCAACTACTACCGCACTTGAACGCTGGTGCTTCCATGCTGCTGCTACAGCTACGCTGAT 1221  
Db 2636 TCCAACTATTATAGAACCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695  
Qy 1222 CAGGATGGGCTGGGCTCCTTGGTGCCCGGCGGAGGGTAGCCATGCTGGGCTGTGTC 1281  
Db 2696 AAGGACTTTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2755  
Qy 1282 CTGGTCTCCGAGTGGGCCATGAGTATATCTTCTGCTTCTGCTTCTGCTTCTTCTTCTTCT 1341  
Db 2756 GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815  
Qy 1342 GTCATGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1401  
Db 2816 GTGCTGTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2875  
Qy 1402 CGCACCAGCGGCGGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461  
Db 2876 CGAAAAAGCGGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2935  
Qy 1462 CAGGTCAGCCTGTACTGCGCAGGAGTGTACGACGCGGCGCTGCTGCTTACCCAGCA 1521  
Db 2936 TTACTGCTTTTATTTCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2995  
Qy 1522 ACTTTCTGGGCGCTGGTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563  
Db 2996 ACATTTTGGATATGTCGCGCACGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3037

Search completed: April 28, 2003, 08:26:02  
Job time : 2971 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1564.2	99.7	2040	21	AAA76170		Human ACAT Related
2	1425.8	90.9	1509	21	AAZ57360		Human acyl CoA:cho
3	1112.4	70.9	1607	21	AAZ57359		Mouse acyl CoA:cho
4	645	41.1	1082	21	AAV01534		Human acylcoenzyme
5	407.2	26.0	4011	15	AAQ63212		Acetyl coenzyme A:
6	404	25.7	3649	19	AAV01536		Human acylcoenzyme
7	394.6	25.1	3650	19	AAT96368		Human acyl-coenzyme
8	191.8	12.2	455	19	AAV01545		Acylcoenzyme A:cho
9	172	11.0	1885	23	ABL13759		Drosophila melanog

PA (UYCO ) UNIV COLUMBIA NEW YORK .





antilipemic; hypercholesterolaemia; hypertriglyceridaemia;  
hyperlipidaemia; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 1..1509  
/\*tag= a  
/product= "ACAT-2"  
/transl\_except= (pos:571..573,aa:Xaa)  
/note= "Xaa is unspecified"

W09967368-A1.

29-DEC-1999.

16-JUN-1999; 99WO-US13683.

23-JUN-1998; 98US-0090354.

08-JUN-1999; 99US-0328857.

(REGC ) UNIV CALIFORNIA.

Cases S, Farese RV, Novak S, Erickson SK;

WPI; 2000-106291/09.

P-PSDB; AAY67953.

Novel polypeptide, useful to treat conditions associated with elevated  
cholesterol ester levels e.g. hypercholesterolemia

Example; Page 52; 57pp; English.

The present sequence encodes the human acyl CoA:cholesterol  
acyltransferase designated ACAT-2. ACAT-2 polypeptides can be  
administered therapeutically, especially by expressing encoding  
polynucleotides, to treat individuals in need of ACAT-2 polypeptide.  
They may especially be administered to treat disease conditions  
associated with elevated cholesterol ester levels e.g.  
hypercholesterolaemia or hyperlipidaemia (including  
hypertriglyceridaemia), since ACAT-2 catalyses the esterification of  
cholesterol with fatty acyl CoA substrates. The polypeptides can also  
be used to diagnose diseases related to polypeptide expression or  
activity, by analysing for polypeptide presence or amount in a sample.  
They are useful to screen for compounds inhibiting or activating the  
polypeptide, which can be included in pharmaceutical compositions and  
administered therapeutically to treat conditions associated with ACAT-2;  
inhibitory agents can especially be used to inhibit ACAT-2 activity,  
especially therapeutically, and especially agents which selectively  
inhibit ACAT-2 and not prior art ACAT-1.

Sequence 1509 BP; 260 A; 457 C; 439 G; 351 T; 2 other;

Query Match 90.9%; Score 1425.8; DB 21; Length 1509;

Best Local Similarity 95.8%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 9; Indels 60; Gaps 1;

1 ATGGAGCCAGCGGGCCCTCTCGCTCGCAGAGGACAGAGGCTGGGAGGGAGCGG 60

1 ATGGAGCCAGCGGGGCCCTCTCGCTCGCAGAGGACAGAGGCTGGGAGGGAGCGG 60

61 GAGCGCCAAACCTGTGGAGATGGAACACTGAGAGCCACAGAGCCCGGACTTGGTACAA 120

61 GAGCGCCAAACCTGTGGAGATGGAACACTGAGAGCCACAGAGCCCGGACTTGGTACAA 120

121 TGGACCGACACATGGAGGCTGTGAGGACACAAATGCTGGAGCAAGCGCAGGACAACTG 180

121 TGGACCGACACATGGAGGCTGTGAGGACACAAATGCTGGAGCAAGCGCAGGACAACTG 180

181 AGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAACTCCATCCATCACAGACAAA 240

181 AGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAACTCCATCCATCACAGACAAA 240

241 CCTCTGCCCCACCTCCCCAGGTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGGAAA 300  
241 CCTCTGCCCCACCTCCCCAGGTTCTTGGAGCAG----- 275  
301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGATGAGTGAGAGTGACAGCATTTC 360  
276 -----TGAGCTGATGGAGTGACAGCATTTC 300  
361 CGCACCATTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCCTGGCC 420  
301 CGCACCATTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCCTGGCC 360  
421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480  
361 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCCACTGATCTTCAGCTTC 420  
481 GGACAGCTGCCATTGGGCTGGTGACCTGGTGCCCATGTTTCTGTCCACCTGTTGGCG 540  
421 GGACAGCTGCCATTGGGCTGGTGACCTGGTGCCCATGTTTCTGTCCACCTGTTGGCG 480  
541 CCGTACCAGGCCCTTACGGCTGTGGCCAGGGGACCTTGGAGCGAGCGGGCTTGGCG 600  
481 CCGTACCAGGCCCTTACGGCTGTGGCCAGGGGACCTTGGAGCGAGCGGGCTTGGCG 540  
601 TGTGCGCTTTTAGCGCCCGCCACGCGTGTGCTCTGCGCGCTGCGCGTCCACGTGGCGGTG 660  
541 TGTGCGCTGTAGCGCCCGCCACGCGTGTGCTGCTGCTGCTTTCGAGCAGGTTAGGTTCC 660  
661 GAGCATCAGCTCCCGCGGCTCCGCTGCTGCTGCTGCTTTCGAGCAGGTTAGGTTCC 720  
601 GAGCATCAGCTCCCGCGGCTCCGCTGCTGCTGCTGCTTTCGAGCAGGTTAGGTTCC 660  
721 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGCGGATCTTCTGCGCAGCAGAGGT 780  
661 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGCGGATCTTCTGCGCAGCAGAGGT 720  
781 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTCTTCTTCTGCCCCAACACT 840  
721 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTCTTCTTCTGCCCCAACACT 780  
841 ATCTACAGGAGACTTACCTTAGGACGCCCTATGCTCAGGTGGATTTATGTCGCAAGAAC 900  
781 ATCTACAGGAGACTTACCTTAGGACGCCCTATGCTCAGGTGGATTTATGTCGCAAGAAC 840  
901 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTGCTTCTTCTTCTTCTGCGCGCTCTGTGT 960  
841 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTGCTTCTTCTTCTTCTGCGCGCTCTGTGT 900  
961 CTGTCTTTGCCAACATGAGCGCGAGGCCCTTTCAGCAGCCCGTGGCTGCTCTCTATC 1020  
901 CTGTCTTTGCCAACATGAGCGCGAGGCCCTTTCAGCAGCCCGTGGCTGCTCTCTATC 960  
1021 CTGCATGCCAGCTGGCCAGGCATCTTCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCT 1080  
961 CTGCATGCCAGCTGGCCAGGCATCTTCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCT 1020  
1081 TGTGCTCAACGCTTTTGGCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAC 1140  
1021 TGTGCTCAACGCTTTTGGCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAC 1080  
1141 TGTGGAACCTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1200  
1081 TGTGGAACCTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1140  
1201 TGGCTGTACAGCTACGTTGATCAGGATGGGCTGCGGCTCTTCTTCTTCTTCTTCTTCTTCT 1260  
1141 TGGCTGTACAGCTACGTTGATCAGGATGGGCTGCGGCTCTTCTTCTTCTTCTTCTTCTTCT 1200  
1261 GTAGCCATGCTGGGTGTGTTCTCCGCACTGCGCCATGAGTATATCTTCTGCTTC 1320  
1201 GTAGCCATGCTGGGTGTGTTCTCCGCACTGCGCCATGAGTATATCTTCTGCTTC 1260  
1321 GTCTGGGGTCTTCTTCTATCCCGTCACTGCTGATCTTCTTCTTCTTCTTCTTCTTCTTCT 1380

Db 1261 GTCTGGGTTCTATCCCGTCATGCTGATACTTCTTCTCATTTGAGGAATGTTG 1320  
 QY 1381 AACTTCATGATGATGACACGACACCGCCCGGCGATGGAACGCTGCTGATGTGGACCATG 1440  
 Db 1321 AACTTCATGATGATGACACGACACCGCCCGGCGATGGAACGCTGCTGATGTGGACCATG 1380  
 QY 1441 CTGTTTCTAGGCGAGGATCCAGTTCAGCTCTACTGCCAGGAGTGGTACGACACGGCGG 1500  
 Db 1381 CTGTTTCTAGGCGAGGATCCAGTTCAGCTCTACTGCCAGGAGTGGTACGACACGGCGG 1440  
 QY 1501 CACTGCCCTTACCCAGGCACTTCTGGGGCTGTGTGACACCTCGACTGCTGCTGCTG 1560  
 Db 1441 CACTGCCCTTACCCAGGCACTTCTGGGGCTGTGTGACACCTCGACTGCTGCTGCTG 1500  
 QY 1561 CATACCTAG 1569  
 Db 1501 CATACCTAG 1509

## RESULT 3

AAZ57359  
ID AAZ57359 standard; cDNA; 1607 BP.

AC AAZ57359;

XX  
DT 05-APR-2000 (first entry)

DE Mouse acyl CoA:cholesterol acyltransferase 2 encoding cDNA.

XX Mouse; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;  
 KW antilipemic; hypercholesterolaemia; hypertriglyceridaemia;  
 KW hyperlipidaemia; ss.

XX Mus musculus.

XX Key Location/Qualifiers  
 FT CDS 30..1607  
 FT /\*tag= a  
 FT /product= "ACAT-2"

XX W09967368-A1.

XX 29-DEC-1999.

XX 16-JUN-1999; 99WO-US13683.

XX 23-JUN-1998; 98US-0090354.

XX 08-JUN-1999; 99US-0328857.

XX (REGC ) UNIV CALIFORNIA.

XX Cases S, Farese RV, Novak S, Erickson SK;

XX WPI; 2000-106291/09.

XX P-PSDB; AAY67952.

XX Novel polypeptide, useful to treat conditions associated with elevated  
 PT cholesterol ester levels e.g. hypercholesterolemia

XX Example; Page 51; 57pp; English.

XX The present sequence encodes the mouse acyl CoA:cholesterol  
 CC acyltransferase designated ACAT-2. ACAT-2 polypeptides can be  
 CC administered therapeutically, especially by expressing encoding  
 CC polynucleotides, to treat individuals in need of ACAT-2 polypeptide.  
 CC They may especially be administered to treat disease conditions  
 CC associated with elevated cholesterol ester levels e.g.  
 CC hypercholesterolemia or hyperlipidaemia (including  
 CC hypertriglyceridaemia), since ACAT-2 catalyses the esterification of  
 CC cholesterol with fatty acyl CoA substrates. The polypeptides can also  
 CC be used to diagnose diseases related to polypeptide expression or  
 CC activity, by analysing for polypeptide presence or amount in a sample.

CC They are useful to screen for compounds inhibiting or activating the  
 CC polypeptide, which can be included in pharmaceutical compositions and  
 CC administered therapeutically to treat conditions associated with ACAT-2;  
 CC inhibitory agents can especially be used to inhibit ACAT-2 activity;  
 CC especially therapeutically, and especially agents which selectively  
 CC inhibit ACAT-2 and not prior art ACAT-1.

XX Sequence 1607 BP; 299 A; 466 C; 456 G; 385 T; 1 other;

QY Query Match 70.9%; Score 1112.4; DB 21; Length 1607;  
 Best Local Similarity 83.2%; Pred. No. 3.7e-267;  
 Matches 1295; Conservative 0; Mismatches 247; Indels 15; Gaps 2;

QY 28 CTCGAGGACAGCAAGGCGCTGGAGGAGCGGAGCGCAACCCCTGT---GCAGATGGA 84  
 Db 51 CTTGGAGGAGAGAGGCGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 110  
 QY 85 AACACTGACAGCAGACAGACCCCGGACCTTGGTACATGATGACCCGACATGAGGCTGTG 144  
 Db 111 AACGCAAGGACACACCGGAACCCCGACACTTGGTGCATGACTCGACATATGGAGGCTGTG 170  
 QY 145 AAGGCACAATTGCTGGAGCAAGCGCAGGAGGACAACTGAGGAGCTGCTGGATCGGCGCATG 204  
 Db 171 AAGACNAGTTTCTGGAGCAAGCAGAGAGAGTGGCAGAGCTGTTGGATCGGGCCCTA 230  
 QY 205 CGGGAGGCTTATAAATCTCTACCATCACAAAGACAAACCTCTGCCCCACCTCCCCAGGT 264  
 Db 231 TGGGAGGCTATCAAGCTTACCCCAACAAAGACAGACCTCTTCCGCTCCGCTGCCAGAT 290  
 QY 265 TCTTTCAGCAGGACCGCAGGAGCCATCCCTGGGGAACAGAAAGTTTTCATATCCGCAAG 324  
 Db 291 TCTACAAGCAAGACCCCGGAGTTACGCCCTGGAAAACGGAAAAGTTTTCGTCGCCGCAAG 350  
 QY 325 TCCCTGCTGATGAGCTGATGAGGTGCAGCATTTCCGACCATCTACCACATGTTTCATC 384  
 Db 351 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 410  
 QY 385 GCTGGCTGTGTGCTTTCATCATCAGCACCCCTGGCCATCGACTTTCATGATGAGGCGAG 444  
 Db 411 GCGGGCTATGTTCTTGTATCATCAGCACCCCTGGCCATCGACTTTCATGATGAGGCGAG 470  
 QY 445 CTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTG 504  
 Db 471 TTGATGCTGGAGTTTGACTTACTCTCTTCAGCTTCGGACAGCTGCCCTTGGCGTGATG 530  
 QY 505 ACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGCGCGGTACACAGCCCTACGCTGTGG 564  
 Db 531 ACCTGGGTGCCCATGTTTCTGTATAGGCTCTTGTAGTGGCTTACACACCTGTGGCTGTGG 590  
 QY 565 GCCA-----GGGGCACCTGGACGACGCGCGGCTGGGCTGTGGCTTTTGA 612  
 Db 591 GCGAGCGCGCGGCTGGGGGTGCTTGGATGCTGGGGGCGAGCTGGGCTTCTGCTG 650  
 QY 613 GCGGCGCGCGGCTGGGCTGCTGCGCGGCTGCGGCTGCGAGTGGCGCTGGAGCATCAGCTC 672  
 Db 651 GCTGCCACGCTGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710  
 QY 673 CGCGCGCGCTCCCGTGTGTCTGCTGCTTCGAGCAGGTTAGTGTCTCTGATGAAAAGCTAC 732  
 Db 711 CGCGCGCGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770  
 QY 733 TCTTTCCTGAGAGGCTGTGCTGGGATCTCTGCTGCGACAGGTTGAGGGATCCAG 792  
 Db 771 TCTTTCCTGAGAGACTGTGCTGGGATCTTGTGTGTCAGACGAGGAAAGGCGCATCAGC 830  
 QY 793 GCCCGCAGTTTCTCCAGCTACTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852  
 Db 831 CCCCAGAGTTTCTCCAGCTACTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 890  
 QY 853 ACTTACCCTAGGACCCCTATGTGCTGAGTGAATTTATGTGGCAAGAACTTTGCCAGGCC 912  
 Db 891 ACATACCCCGAGGACACCCAGCATCAGTGGAACTATGTGGCAAGAACTTTGCCAGGCC 950



QY 1441 CTGTTTCTAGCCAGGAATCCAGGTACGCTGTACTGCCAGAGTGTGTACGACGGGG 1500  
 |||||  
 Db 544 CTGTTTCTAGCCAGGAATCCAGGTACGCTGTACTGCCAGAGTGTGTACGACGGGG 603  
 |||||  
 QY 1501 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 1560  
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 Db 604 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 663  
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 QY 1561 CATACCTAG 1569  
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 Db 664 CATACCTAG 672  
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RESULT 5  
 ID AAQ63212 standard; cDNA; 4011 BP.  
 AC AAQ63212;  
 XX  
 DT 03-JAN-1995 (first entry)  
 XX  
 DE Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).  
 XX  
 KW Acetyl coenzyme A: cholesterol acetyltransferase; ACAT; disease;  
 KW diagnosis; detection; screening; treatment; prophylaxis;  
 KW hypercholesterolaemia; atherosclerosis; antisense; probe;  
 KW identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT 1397..3049  
 FT CDS  
 FT /tag= a  
 FT /product= Acetyl CoA: cholesterol acetyltransferase  
 FT polyA\_signal  
 FT 3385..3389  
 FT /tag= b  
 FT /note= "Putative polyadenylation signal."  
 FT polyA\_signal  
 FT 3962..3967  
 FT /tag= c  
 FT /note= "Putative polyadenylation signal."  
 FT  
 XX  
 XX WO9409126-A.  
 XX  
 XX 28-APR-1994.  
 XX  
 XX 12-OCT-1993; 93WO-US09704.  
 XX  
 XX 14-OCT-1992; 92US-0959950.  
 XX  
 XX 10-SEP-1993; 93US-0121057.  
 XX  
 XX (DART-) DARTMOUTH COLLEGE.  
 XX  
 XX Chang CCY, Chang T;  
 XX  
 XX WPI; 1994-151312/18.  
 XX  
 XX P-PSDB; AAR53079.  
 XX  
 XX Acetyl coenzyme A: cholesterol acetyltransferase and nucleic  
 XX acid sequence encoding it - used to correct enzyme deficiencies  
 XX and screen for enzyme inhibitors  
 XX  
 XX Claim 13; Figure 9; 52pp; English.  
 XX  
 XX The acetyl coenzyme A: cholesterol acetyltransferase (ACAT) gene  
 XX sequence enables the screening of human populations for abnormal  
 XX human ACAT activities for disease diagnosis. It provides  
 XX information concerning the catalytic mechanism of ACAT and allows  
 XX the design of drugs serving as specific ACAT inhibitors, desirable  
 XX for the prevention and/or treatment of human hypercholesterolaemia  
 XX and human atherosclerosis. It also allows the design of antisense  
 XX cDNAs or RNAs to inhibit ACAT production, or probes to identify  
 XX different forms of human ACAT or ACAT from different animal species.

CC This sequence is a human ACAT cDNA sequence designated K1.  
 XX  
 SQ Sequence 4011 BP; 1056 A; 793 C; 839 G; 1323 T; 0 other;  
 Query Match 26.0%; Score 407.2; DB 15; Length 4011;  
 Best Local Similarity 59.0%; Pred. No. 2.8e-91;  
 Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;  
 QY 287 CATCCCTCGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGATGAGCTGATGG 346  
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 Db 1737 CACCTCCAGAACAGAAAGATTTTATGCAAGCGCTCTCTCTAGTAGAAGTCTG 1796  
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 QY 347 AGGTGACAGATTTCGACCATCTACACATGTTTCATCGTGGCCCTGTGTGTTTCATCA 406  
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 Db 1797 AAGTGGACCATCAGAACATATATACATGTTTATGGCCCTCCTATCTCTTTATCC 1856  
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 QY 407 TCAGCACCTTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGGAGTTGACCTAC 466  
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 Db 1857 TCAGCACACTTGTAGTAGATTACATTTGATGAAGGAGGCTGGTGTGATGACCTCC 1916  
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 QY 467 TGATCTTCAGCTTCGACAGCTGCCATTGGCGCTGGTACCTGGGTGCCCATGTTTCTGT 526  
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 Db 1917 TGTCTTATGCTTTTGGCAATTTCTACCGTGTGTTGGACCTGGTGGATCATGTTCTGT 1976  
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 QY 527 CCACCTGTGGCGCGGTACACAGCCCTACGGCTGTGGCCAGGGGACCTGGAGCAGG 586  
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 Db 1977 CTACATTTTTCAGTCCCTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGTT 2036  
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 QY 587 CGACGGGCTGGCTGTGGCTTTTAGCGGCCACCGCTGGTGTGCTGCGGCTGCCGG 646  
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 Db 2037 CTCATCCGCTGATCCGTTCTCTTCCATGGCTTTCTTTTCATGATTTCCAGATTGGAG 2096  
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 QY 647 TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGGGCTCCCTT 688  
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 Db 2097 TTCTAGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGGT 2156  
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 QY 689 GTGCTCTGTTCGACGAGTTAGTTCCTGATGAAGAGTACTCTCTCTCTGACAGAGG 748  
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 Db 2157 TCATCATTTATTCGACGAGATTCGTTTGTAAAGGCCCACTCATTTGTGACAGAGA 2216  
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 QY 749 CTGCTCGGGATCTCTGTCGACAGAGGTGAGGGGATCCAGGCCCACTTCTCCA 808  
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 Db 2217 ACCTGCTCGGGTACTAAT-TCAGTAGAGAAATCAAGCACTGTTCATATAGCTACA 2275  
 |||||  
 QY 809 G-----CTACCTCTACTTCTCTTCTGCCAACACTATCTACAGGAGACTTACCT 861  
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 Db 2276 GTCAACACGATTTGTACTTCTTATTTGCTCTACCTTATCTACCGTGACAGTACCC 2335  
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 QY 862 AGGAGCCCTATGTCAGTGGAAATTTATGCGCAAGAACTTTGCCAGGCCCTGGATGT 921  
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 Db 2336 AGGAATCCCACTGTAAGATGGGGTTATGTCGTATGAAGTTTGCACAGCTTTTGGTGC 2395  
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 QY 922 GTGCTCTATGCTGCTTCATCTCGGGCCCTCTGTGTTCTCTCTTTGCCAACATGAGC 981  
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 Db 2396 TTTTCTATGCTACTACATCTTTGAAAGGCTTTGGCCCTCTGTTTGGGAATATCAA 2455  
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 QY 982 CGAGAGCCCTTCAGCACCCGTCCTGTGTCTCTATCTGCTGCATGCCACGTTGCCAGGC 1041  
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 Db 2456 CAGGAGCCCTTCAGGCGCTGCTGTTCTGTGCTCTATGTTTAACTCCATCTTGGCAGT 2515  
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 QY 1042 ATCTTCATGCTGCTGCTCATCTCTTCTGCTTCCCTCCATGCTGCTGCTCAACGCCTTGCC 1101  
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 Db 2516 GTGCTGATTTCTTCTTACTTTTGTGCTTTTGGCACTGCTGGCTCAATGCCTTTGT 2575  
 |||||  
 QY 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGCTCTTC 1161  
 |||||  
 Db 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAGGATTTGGGAACTCCACGTCATAC 2635  
 |||||  
 QY 1162 TCCAACTACTACCGCACTTTGGAACGTTGGTGGTCCATGATGCTGCTGTACAGTACGTGAT 1221  
 |||||  
 Db 2636 TCCAACTATTATAGAACCTGGAATGTTGGTGGTCCATGACTGGCTATATTACTATGCTTAC 2695  
 |||||  
 QY 1222 CAGGATGGGCTGGGCTCTCTTGTGCTGCCCGGCCGAGGAGTAGCCATGCTGGTGTGTTTC 1281  
 |||||

Db 2696 AAGGACTTTCTCTGGTTTCTTCCAGAGATTCAAATCTCTGCGCATGTTAGCTGTCTTT 2755  
Qy 1282 CTGGTCTCCGAGTGGCCATGAGTATATCTTCTGCTCTGCTGCTGGGTTCTTCTATCCC 1341  
Db 2756 GCTGTATCTCTGTAGTACAGAAATGCGCTGGCTGTTGCTTGAGCTTTTCTATCCC 2815  
Qy 1342 GTATGCTGATCTCTTCCCTGTTCATTTGGAGGAATGTTGAATCTCATGATGATGACGAG 1401  
Db 2816 GTGCTGTTCTGCTCTTCATGTTCTTTGGAAATGGCTTTCAACTTCATGTTCAATGATAGT 2875  
Qy 1402 CGACCGGCGCCGATGGAAGCTGTGATGTGACCAATGCTGTTTTCAGGCCAGGGAATC 1461  
Db 2876 CGAAAAAGCCGATTTGGAATGTTCTGATGTGACATTTCTTTTCTTTGGGCAATGGAGTC 2935  
Qy 1462 CAGTCAAGCTGTACTGCCAGGAGTGTACGCGGCGGACCTGCCCTTACCCAGGCA 1521  
Db 2936 TTACTGCTGCTTTTATCTCAAGAAATGATGACGCTGGGACATGCTCTCTGAAAAATCCC 2995  
Qy 1522 ACTTTCTGGGGCTGTGACACCTCGATCTTGGTCTCGCCAT 1563  
Db 2996 ACATTTTGGATTATGTCGCGCCAGGTTCTCGGACTTGTGCT 3037

## RESULT 6

AAV01536

ID AAV01536 standard; DNA: 3649 BP.

XX AC AAV01536;

XX DT 08-JUN-1998 (first entry)

XX DE Human acylcoenzyme A:cholesterol acyltransferase (ACAT I) DNA.

XX KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;

XX KW ACAT related gene product 1; ARGP-1; ARGP-2; sterol esterification;

XX KW Inhibitor; atherosclerosis; hyperlipidaemia; human; ss.

XX OS Homo sapiens.

XX PH Key

XX FT CDS

XX FT 1397..3049

XX FT /\*tag= a

XX PN WO9745439-A1.

XX PR 04-DEC-1997.

XX PR 30-MAY-1997; 97WO-US09460.

XX PR 30-MAY-1996; 96US-0657620.

XX PR (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Sturley SL;

XX PI WPI; 1998-032573/03.

XX DR P-PSDB; AAW43409.

XX XX

XX PT DNA encoding acylcoenzyme A: cholesterol acyltransferase II or

XX PT III - useful to identify inhibitors for treatment of

XX PT atherosclerosis or hyperlipidaemia

XX XX

XX PS Disclosure; Fig 5A 1-3; 121pp; English.

XX CC This nucleic acid molecule encodes human acylcoenzyme A:cholesterol

XX CC acyltransferase (see AAW43409), or ACAT I. The invention relates to

XX CC isolated nucleic acids (see AAV01533-35), coding for human and mouse

XX CC acylcoenzyme A:cholesterol acyltransferase II and III (see

XX CC AAW43406-08), also designated ACAT related gene products (ARGP) I

XX CC and 2. These can be used to identify inhibitors useful in the

XX CC treatment of atherosclerosis and hyperlipidaemia.

XX XX

SQ Sequence 3649 BP; 929 A; 749 C; 781 G; 1190 T; 0 other;  
Query Match 25.7%; Score 404; DB 19; Length 3649;  
Best Local Similarity 58.8%; Pred. No. 1.7e-90;  
Matches 766; Conservative 0; Mismatches 510; Indels 26; Gaps 3;  
Qy 287 CATCCCTGGGGAACAGAAAAGTTTTCATCATCGCAAGTCCCTGCTGTGAGTGTGCTGTATCA 346  
Db 1737 CACTCCAGAACAAAGAAAGATTTTATTGCAAGCGCTCTCTCTTAGATGAACATGCTTG 1796  
Qy 347 AGGTGAGCATTTCCCGACCATCTACACATGTTTCATCGCTGGCTGTGCTGTATCA 406  
Db 1797 AAGTGGACCATCATAGAACAAATATATCATGTTTATTGGCTCTCTCATCTCTTTATCC 1856  
Qy 407 TCAGCACCTTGGCCATCGACTTTCATGATGAGGACGCTGCTGCTGGAGTTTTCACCTAC 466  
Db 1857 TCAGCACCTTGTAGTAGATTACATGATGAAGAAAGCTGGTGGTGTGAGTTTCAGCTCC 1916  
Qy 467 TGATCTTCAGCTTGGGACAGCTGCCATTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 526  
Db 1917 TGTCTTATGCTTTTGGCAAAATTTCTACCGTTGTTGGACCTGGTGGATCATGTTCTGT 1976  
Qy 527 CCACCTGTTGGCGCGCTACAGGCCCTACGGCTGTGGCGCAGGCGCACCTGGAGCAGG 586  
Db 1977 CTACATTTTCAGTTCCCTATTTTCTGTTCAACATTTGGCGACATGCTATAGCAAGAGTT 2036  
Qy 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGGCCACCGCGTGGTGGTGGTGGTGGTGGTGGTGG 646  
Db 2037 CTCATCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG 2096  
Qy 647 TCC-----ACGTGGCGGTGGAGCATACAGTCCCGCGGCTCCCGCTCCCGTT 688  
Db 2097 TTCTAGGTTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGGT 2156  
Qy 689 GTGCTCTGCTTCGACGAGGTTAGTCTCTGTAGTAAAGCTACTCTCTCTCTCTGAGAGAGG 748  
Db 2157 TCATCATATATTCGACGAGATTCGTTTGTAAATGAGGCGCCACTCATTTGTTCAGAGAGA 2216  
Qy 749 CTGTGCTGGGATCCTTCGTGCCAGAGAGGTGAGGGGATCCAGGCCCCCAGTTTCTTCCA 808  
Db 2217 ACGTGCTCGGGTACTAAAT-TCAGCTAAGAGAGAAATCAAGCACTGTTTCCAATACCTACA 2275  
Qy 809 G-----CTACCTCTACTCTCTTCTGCGCAACACATCATCTACAGGAGACATTCCT 861  
Db 2276 GTCAACCAAGTATTTGTTACTTCTTATTTGCTCTACCTCTATCTACCTGACAGCTATCCC 2335  
Qy 862 AGGAGCGCTTATGTCAGTGGAAATATGTGGCAAGAACTTTGCGCCAGGCGCTGGGATGT 921  
Db 2336 AGAATCCCACTGTAAGATGGGTTATGTCGTATGAAGTTTGGACAGGCTTTTGGTTGC 2395  
Qy 922 GTGCTCTATGCTCTTCTATCCTCTGGCGGCTCTGTGTTCTGTTTTCGCAACATGAGC 981  
Db 2396 TTTTCTCTATGTTACTACATCTTTGAAAGGCTTTGTGCCCCCTTTGTTGCGAATATCAA 2455  
Qy 982 CGAGAGCCCTTCAGCACCGCTGGTCTCTCTATCTCTGATGCAATGCCAGCTTCCAGGC 1041  
Db 2456 CAGGAGCCCTTCAGCGCTCGTGTCTGTCTCTATGTTTAACTCCATCTTCCAGGT 2515  
Qy 1042 ATCTTCTATGCTGCTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101  
Db 2516 GTGCTGATCT 2575  
Qy 1102 GAGATGCTAGCATTTGGAGCAGGATGTTCTACCGGACTGTGGAACTCAACCTCTCTCTCT 1161  
Db 2576 GAGATGTTACGCTTTGGTACAGAGATGTTCTATGAAGATTTGGTGAAGTCCACCTCATAC 2635  
Qy 1162 TCCAACTACTACCGCTTGGACGCTGGTGGTCCATGACTGGCTGTACAGCTACGCTGTAT 1221  
Db 2636 TCCAACTATTATAGAACCTGGAATGTTGGTGTCCATGACTGGCTATATTACTATGCTTAC 2695  
Qy 1222 CAGATGGGCTGGGCTCTCTTGTGTCGCGGCGGCGGAGGAGTACGCTGGTGGTGGTGGT 1281  
Db 2696 AAGGACTTTCTCTGTTTCTTCTCCAAAGAGATTTCAAATCTGTCGCTATGTTAGTGTCTTT 2755











## RESULT 12

AAQ63210  
 ID AAQ63210 standard; cdNA; 996 BP.  
 AC  
 AAQ63210;  
 DT  
 03-JAN-1995 (first entry)  
 XX Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).  
 DE  
 XX Acetyl coenzyme A: cholesterol acetyltransferase; ACAT; disease;  
 KW diagnosis: detection; screening; treatment; prophylaxis;  
 KW hypercholesterolaemia; atherosclerosis; antisense; probe;  
 KW identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09409126-A.  
 XX  
 PD 28-APR-1994.  
 XX  
 XX 12-OCT-1993; 93WO-US09704.  
 PF  
 XX 14-OCT-1992; 92US-0959950.  
 PR 10-SEP-1993; 93US-0121057.  
 XX  
 XX (DART-) DARTMOUTH COLLEGE.  
 PA  
 XX Chang CCY, Chang T;  
 PI  
 XX WPI; 1994-151312/18.  
 DR  
 XX  
 XX Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic  
 PT acid sequence encoding it - used to correct enzyme deficiencies  
 PT and screen for enzyme inhibitors  
 XX  
 PS Claim 13; Figure 3; 52pp; English.  
 XX  
 CC The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene  
 CC sequence enables the screening of human populations for abnormal  
 CC human ACAT activities for disease diagnosis. It provides  
 CC information concerning the catalytic mechanism of ACAT and allows  
 CC the design of drugs serving as specific ACAT inhibitors, desirable  
 CC for the prevention and/or treatment of human hypercholesterolaemia  
 CC and human atherosclerosis. It also allows the design of antisense  
 CC DNAs or RNAs to inhibit ACAT production, or probes to identify  
 CC different forms of human ACAT or ACAT from different animal species.  
 CC This sequence is a human ACAT cDNA clone designated C1.  
 XX  
 SQ Sequence 996 BP; 258 A; 219 C; 207 G; 312 T; 0 other;

Query Match 8.6%; Score 134.6; DB 15; Length 996;  
 Best Local Similarity 53.1%; Pred. No. 1.4e-23;  
 Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;  
 QY 287 CATCCCTGGGGAACAGAAAGTTTCATCCGACGTCCTCGAGTCCCTGCTGATGAGCTCATGG 346  
 DB 262 CACCTCCAGAACAGAAAGATTTTATTGCAAGCGCTCTCTCTTAGATGAAGTCTGTTG 321  
 QY 347 AGGTGCAGCATTTCCGCGACCATACACATGTTATCGTGGCGCTGCTGCTTCATCA 406  
 DB 322 AAGTGGACCATACACACATATATACATGTTTATTCCTCCCTCATCTCTTTATCC 381  
 QY 407 TCAGCACCTGGCCATCGACTTCATGATGAGGCGAGGCTGCTGG--AGTTTGACCT 464  
 DB 382 TCAGCACACTGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441  
 QY 465 ACTG-ATCTTCAGTTCGACAGCTGCCATGCGCGTGGTACCTGGGTCGCAATGTTTC 523  
 DB 442 CTTGCTTATGCAATTTGGCAATTTCTTACCGTTGTTTGGACCTGGTGGATCATGTTCC 501  
 QY 524 TGTCACCTGTTGGCGCGGTACACAGGCGCTACGGCTGTGGCGGACGGCACCTGGACGC 583

DB 502 TGCTACATTTTCAGTTCCTATTTTCTGTTTCAACATTTGGCGACTGGCTATAGCAAGA 561  
 QY 584 AGCGGACGGGCTGGCTGTGGCGCTTTTAGCGCGCCACGCGGTGGTCTC----- 633  
 DB 562 GTTCTCATCGCGTATCCGTTCTCTCTTCATCGCTTTCTTTTCATGATTTCCAGATTG 621  
 QY 634 ---TGCGCGCTGCCGCTGCACGTTGGCGGTGGAGCATCAGTCCCGCGGCTCCCGTGT 690  
 DB 622 GAGTTCTAGTTTGGACCAACATATGTTGTTAGCATATCTGCCACCATGTTCCCGG 681  
 QY 691 GTCTCTGCTTCGACGAGTTAGTTCCTCATGAAAGCTACTCTCTCTCGAGAGGCT 750  
 DB 682 TTCTCATATTCGACGAGATGTTTGTAAATGAAGGCCCACTCATTTGTCAGAGAAC 741  
 QY 751 GTGCTGGGATCCTTCTGTCGACGAGGTGAGGGATCCAGGCC-----CCAGTTTCT 805  
 DB 742 GTGCTCGGTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACAGTCA 801  
 QY 806 CCAGCTACCTCTACTTCTCTTCTGCGCAACACTATCTACAGGAGACTTACCCCTAGGA 865  
 DB 802 ACCAGTATTTGTACTTCTTATTTGCTCTACCTTATCTACCGTGACAGCTATCCAGGA 861  
 QY 866 CGCCTATGTCAGTGGAAATATGTGCCAAGAACTTTGCCAGGCCCTGGGATGTGTC 925  
 DB 862 ATCCCACTGTAGATGGGTTATGTTGCTATGAAGTTTGCACAGGCTTTGGTGTCTTT 921  
 QY 926 TCTATGCTCTCTCTCTGCGCGCTCTGTGTTCTCTCTGTTTGGCAACATCAGCGGAG 985  
 DB 922 TCTATGTTACTACTTCTTTGAAAGGCTTTGTGCCCCCTGTTTCGGAATATCAACAGG 981  
 QY 986 AGCCCTTCAGACCC 1000  
 DB 982 AGCCCTTCAGCGCTC 996  
 RESULT 13  
 AA001539  
 ID AA001539 standard; cdNA; 983 BP.  
 AC AA001539;  
 DT 08-JUN-1998 (first entry)  
 XX Human acylcoenzyme A:cholesterol acyltransferase II (ACAT II), DNA.  
 DE  
 KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;  
 KW ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;  
 KW inhibitor; atherosclerosis; hyperlipidaemia; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..660  
 FT /\*tag= a  
 XX  
 PN W09745439-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 XX 30-MAY-1997; 97WO-US09460.  
 XX  
 XX 30-MAY-1996; 96US-0657620.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX Sturley SL;  
 PI  
 XX WPI; 1998-032573/03.  
 DR P-PSDB; AAW43412.  
 DR  
 XX DNA encoding acylcoenzyme A: cholesterol acyltransferase II or  
 PT III - useful to identify inhibitors for treatment of  
 PT atherosclerosis or hyperlipidaemia

[illegible]

PR 20-OCT-2000; 2000US-241785P.  
PR 20-OCT-2000; 2000US-241786P.  
PR 20-OCT-2000; 2000US-241787P.  
PR 20-OCT-2000; 2000US-241808P.  
PR 20-OCT-2000; 2000US-241809P.  
PR 20-OCT-2000; 2000US-241826P.  
PR 01-NOV-2000; 2000US-244617P.  
PR 08-NOV-2000; 2000US-246474P.  
PR 08-NOV-2000; 2000US-246475P.  
PR 08-NOV-2000; 2000US-246476P.  
PR 08-NOV-2000; 2000US-246477P.  
PR 08-NOV-2000; 2000US-246478P.  
PR 08-NOV-2000; 2000US-246523P.  
PR 08-NOV-2000; 2000US-246524P.  
PR 08-NOV-2000; 2000US-246525P.  
PR 08-NOV-2000; 2000US-246526P.  
PR 08-NOV-2000; 2000US-246527P.  
PR 08-NOV-2000; 2000US-246528P.  
PR 08-NOV-2000; 2000US-246532P.  
PR 08-NOV-2000; 2000US-246609P.  
PR 08-NOV-2000; 2000US-246610P.  
PR 08-NOV-2000; 2000US-246611P.  
PR 08-NOV-2000; 2000US-246613P.  
PR 17-NOV-2000; 2000US-249207P.  
PR 17-NOV-2000; 2000US-249208P.  
PR 17-NOV-2000; 2000US-249209P.  
PR 17-NOV-2000; 2000US-249210P.  
PR 17-NOV-2000; 2000US-249211P.  
PR 17-NOV-2000; 2000US-249212P.  
PR 17-NOV-2000; 2000US-249213P.  
PR 17-NOV-2000; 2000US-249214P.  
PR 17-NOV-2000; 2000US-249215P.  
PR 17-NOV-2000; 2000US-249216P.  
PR 17-NOV-2000; 2000US-249217P.  
PR 17-NOV-2000; 2000US-249218P.  
PR 17-NOV-2000; 2000US-249244P.  
PR 17-NOV-2000; 2000US-249245P.  
PR 17-NOV-2000; 2000US-249264P.  
PR 17-NOV-2000; 2000US-249265P.  
PR 17-NOV-2000; 2000US-249297P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 17-NOV-2000; 2000US-249300P.  
PR 01-DEC-2000; 2000US-250160P.  
PR 01-DEC-2000; 2000US-250391P.  
PR 05-DEC-2000; 2000US-251030P.  
PR 05-DEC-2000; 2000US-251988P.  
PR 05-DEC-2000; 2000US-256719P.  
PR 06-DEC-2000; 2000US-251479P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
PR 08-DEC-2000; 2000US-251989P.  
PR 08-DEC-2000; 2000US-251990P.  
PR 11-DEC-2000; 2000US-254097P.  
PR 05-JAN-2001; 2001US-259678P.  
(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476161/51.

DR P-PSDB; ABB10191.

XX Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
PT condition

PS Claim 1; SEQ ID NO: 79; 859pp + Sequence Listing; English.

XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs, these can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence

CC is a cDNA of the invention.

XX Sequence 993 BP; 218 A; 260 C; 328 G; 186 T; 1 other;  
SQ

Query Match 6.1%; Score 95; DB 22; Length 993;  
Best Local Similarity 58.7%; Pred. No. 1e-13;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCAGCTTGGCCAGGCATCTTTCATCTGCTGCTTCCTTTGCTTCTCTCC 1078  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 780 TCCTGAAGCTGGCGGTCCTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGCTCTCC 721  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1079 ATTGCTGGCTCAACGCTTTGCCGAGATGCTACGATTTGGAGACAGAGATTTCTACCGGG 1138  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 720 ACTCCTGCCTGAATGCCGTGGCTGAGCTCAGTTTGGAGACCGGAGTTCTACCGGG 661  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1139 ACTGGTGGAACTCAACGCTCTTCTCCAACTACTACGCACCTGGAACTGGTGGTGCATG 1198  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 660 ACTGGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTTGTGCACA 601  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGCTGCGGCTCCTTGTGCGCGGCCGAG 1258  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 600 AGTGGTGCATCAGACACACTTCTACAAGCCCATGCTTCGAC-----GGGCAGCAGAAGT 547  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1259 GGTAGCCATGCTGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1318  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 546 GGATGGCCAGGACAGGGGTGCTTCTGCGCTGCGGCTTCTTCCACGAGTACCTGGTGAGCG 487  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1319 TCGTCTCTGGGTTCTTC 1335  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 486 TCCCTCTGCGAATGTTTC 470  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

#### RESULT 15

AAV01533

ID AAV01533 standard; DNA; 1521 BP.

XX AC AAV01533;

XX DT 08-JUN-1998 (first entry)

XX Human acylcoenzyme A:cholesterol acyltransferase II DNA.

XX Acylcoenzyme A:cholesterol acyltransferase II; ARGP-1;

KW ACAT related gene product 1; human; sterol esterification;

KW inhibitor; atherosclerosis; hyperlipidaemia; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1224

FT /\*tag= a

XX WO9745439-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US09460.

XX PR 30-MAY-1996; 96US-0657620.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Sturley SL;

XX WPI; 1998-032573/03.

DR P-PSDB; AAW43406.

XX DNA encoding acylcoenzyme A: cholesterol acyltransferase II or

PT III - useful to identify inhibitors for treatment of

PT atherosclerosis or hyperlipidaemia

XX Claim 5; Fig 15A-B; 121pp; English.

PS

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Job time : 308 secs

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 05:47:38 ; Search time 53 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1564.2	99.7	2040	3	US-09-165-042-4
2	405.6	25.9	4011	1	US-08-121-057-3
3	405.6	25.9	4011	2	US-08-509-187D-3
4	405.6	25.9	4011	2	US-09-121-396-3
5	405.6	25.9	4011	5	PCT-US93-09704A-3
6	359.8	22.9	4079	1	US-08-121-057-2
7	359.8	22.9	4079	2	US-08-509-187D-2
8	359.8	22.9	4079	2	US-09-121-396-2
9	359.8	22.9	4079	5	PCT-US93-09704A-2
10	134.6	8.6	996	1	US-08-121-057-1
11	134.6	8.6	996	2	US-08-509-187D-1
12	134.6	8.6	996	2	US-09-121-396-1
13	134.6	8.6	996	5	PCT-US93-09704A-1
14	95	6.1	1895	4	US-09-326-203A-14
15	95	6.1	1976	3	US-09-165-042-2
16	81.4	5.2	1650	4	US-09-103-754A-2
17	79.8	5.1	1766	4	US-09-326-203A-15
18	79.8	5.1	1766	4	US-09-326-203A-16
19	56.8	3.6	7218	1	US-08-232-463-14
20	55.4	3.5	519	4	US-09-326-203A-11
21	50	3.2	1942	4	US-09-326-203A-1
22	42	2.7	3358	3	US-09-248-571-2
23	42	2.7	3358	4	US-09-553-736-2
24	41.2	2.6	7218	1	US-08-232-463-14
25	40	2.5	629	4	US-09-103-754A-3
26	39.8	2.5	2970	4	US-09-110-517-3
27	39.8	2.5	5173	1	US-08-242-677-1

28	39.4	2.5	20235	1	US-07-642-734C-3	Sequence 3, Appli
29	39.4	2.5	20235	3	US-08-439-009A-3	Sequence 3, Appli
30	39.2	2.5	1469	5	PCT-US92-08258-1	Sequence 1, Appli
31	39.2	2.5	2353	5	PCT-US92-08840-1	Sequence 1, Appli
32	39	2.5	289	4	US-09-007-005-17	Sequence 17, Appli
33	39	2.5	289	4	US-09-244-796-17	Sequence 2, Appli
34	39	2.5	2474	4	US-08-666-392A-2	Sequence 2, Appli
35	39	2.5	2474	4	US-09-199-926-2	Sequence 3, Appli
36	39	2.5	33529	4	US-09-144-085-3	Sequence 3, Appli
37	38.8	2.5	30001	1	US-08-125-468-1	Sequence 1, Appli
38	38.8	2.5	30001	2	US-08-474-933-1	Sequence 1, Appli
39	38.6	2.5	2080	2	US-08-878-563A-2	Sequence 2, Appli
40	38.6	2.5	2080	4	US-09-270-117-2	Sequence 2, Appli
41	38.6	2.5	2430	4	US-09-105-537-23	Sequence 23, Appli
42	38.6	2.5	13613	4	US-09-105-537-3	Sequence 3, Appli
43	38.4	2.4	500	3	US-09-141-000-2	Sequence 2, Appli
44	38.4	2.4	696	4	US-09-461-697-193	Sequence 193, App
45	38.4	2.4	699	4	US-09-461-697-191	Sequence 191, App

ALIGNMENTS

RESULT 1  
US-09-165-042-4  
; Sequence 4, Application US/09165042  
; Patent No. 6100077  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331  
; CURRENT APPLICATION NUMBER: US/09/165,042  
; CURRENT FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-165-042-4

Query Match	99.7%	Score 1564.2;	DB 3;	Length 2040;
Best Local Similarity	99.8%	pred. No. 0;		
Matches 1566;	Conservative	0;	Mismatches	3;
			Indels	0;
			Gaps	0;
Qy	1	ATGAGCCAGCGGGGGCCGCTCTCGCTGCAGAGGACAGAGGGCTGGGAGGGAGCGG	60	
Db	52	ATGAGCCAGCGGGGGCCGCTCTCGCTGCAGAGGACAGAGGGCTGGGAGGGAGCGG	111	
Qy	61	GAGGCCAACCCCTGTGAGATGGAACACCTGAGACGACAGAGCCCGGACTTGGTACAA	120	
Db	112	GAGGCCAACCCCTGTGAGATGGAACACCTGAGACGACAGAGCCCGGACTTGGTACAA	171	
Qy	121	TGGACCCGACACATGAGGCTGTGAAGCCACAATTTGTTGGAGCAAGCGCAGGACAAC	180	
Db	172	TGGACCCGACACATGAGGCTGTGAAGCCACAATTTGTTGGAGCAAGCGCAGGACAAC	231	
Qy	181	AGGAGCTGTGATCGGGCCATCGGGAGGCTATACAATCCTTACCCTACACAGACAAA	240	
Db	232	AGGAGCTGTGATCGGGCCATCGGGAGGCTATACAATCCTTACCCTACACAGACAAA	291	
Qy	241	CTCTGCCCCACCTCCCGGAGTTCCTTGGAGGAGCCAGGAGCCATCCCTGGGGAAA	300	
Db	292	CTCTGCCCCACCTCCCGGAGTTCCTTGGAGGAGCCAGGAGCCATCCCTGGGGAAA	351	
Qy	301	CAGAAAGTTTTCATCATCCCAAGTCCCTGCTGATGAGCTGATGAGGTGCAGCATTTTC	360	
Db	352	CAGAAAGTTTTCATCATCCCAAGTCCCTGCTGATGAGCTGATGAGGTGCAGCATTTTC	411	
Qy	361	CGCACCATCTACACATGTTTCATCGCTGGCTGTGTCTTCATCATCAGCACCCTGCC	420	
Db				

Db 412 CGACACATCTACACATGTTTCATCGCTGGCTGTGTCTTCATCATCAGCACCTCTGGCC 471  
Qy 421 ATCGACTTATGATGAGGAGAGCTGCTGTGTGAGTTTGACCTTACTGATCTTCACTTC 480  
Db 472 ATCGACTTATGATGAGGAGAGCTGCTGTGTGAGTTTGACCTTACTGATCTTCACTTC 531  
Qy 481 ATCGACTTATGATGAGGAGAGCTGCTGTGTGAGTTTGACCTTACTGATCTTCACTTC 540  
Db 532 GGACAGCTGCCATTTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 591  
Qy 541 CCGTACAGGAGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 600  
Db 592 CCGTACAGGAGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 651  
Qy 601 TGTGCGGTTTATGAGGAGAGCTGCTGTGTGAGTTTGACCTTACTGATCTTCACTTC 660  
Db 652 TGTGCGGTTTATGAGGAGAGCTGCTGTGTGAGTTTGACCTTACTGATCTTCACTTC 711  
Qy 661 GAGCATCAGCTTCCCGGCGGCTTCCCGTGTGTGTGCTTCTTCCGAGAGGTTAGTTCCTG 720  
Db 712 GAGCATCAGCTTCCCGGCGGCTTCCCGTGTGTGTGCTTCTTCCGAGAGGTTAGTTCCTG 771  
Qy 721 ATGAAAGCTACTCTTCTTCTGAGAGGCTGTGCTTGGGATCTTCTTCCGAGAGAGT 780  
Db 772 ATGAAAGCTACTCTTCTTCTGAGAGGCTGTGCTTGGGATCTTCTTCCGAGAGAGT 831  
Qy 781 GAGGAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 951  
Db 832 GAGGAGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891  
Qy 841 ATCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
Db 892 ATCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 951  
Qy 901 TTTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
Db 952 TTTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1011  
Qy 961 CTGCTGCTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
Db 1012 CTGCTGCTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071  
Qy 1021 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
Db 1072 CTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1131  
Qy 1081 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
Db 1132 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1191  
Qy 1141 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
Db 1192 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1251  
Qy 1201 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
Db 1252 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1311  
Qy 1261 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
Db 1312 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1371  
Qy 1321 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
Db 1372 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1431  
Qy 1381 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
Db 1432 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1491  
Qy 1441 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Db 1492 TGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1551

Qy 1501 CACTGCCCTTACCCAGGCAACTTCTCTGGGGCTGGTGACACCTCGATCTTGGTCTGC 1560  
Db 1552 CACTGCCCTTACCCAGGCAACTTCTCTGGGGCTGGTGACACCTCGATCTTGGTCTGC 1611  
Qy 1561 CATACCTAG 1569  
Db 1612 CATACCTAG 1620

RESULT 2  
US-08-121-057-3  
; sequence 3, Application US/08121057  
; Patent No. 5484727  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, CATHERINE C. Y.  
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: ASCII text  
; CURRENT RELEASE DATE:  
; FILING DATE: 05/08/121.057  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAMPORT HAMMITTE, ANN.  
; REGISTRATION NUMBER: 34,858  
; REFERENCE/PACKET NUMBER: DCI-033CP  
; TELEPHONE: (617) 227-2700  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4011 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE TYPE: CDS  
; NAME/KEY: CDS  
; LOCATION: 1397..3046  
; US-08-121-057-3

Query Match 25.9%; Score 405.6; DB 1; Length 4011;  
Best Local Similarity 58.9%; Pred. No. 1.1e-94;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

Qy 287 CACTCCTGGGAACAGAAAGTTTATTGCAAGCGCTCTCTTAGATGAACCTGTTG 1796  
Db 1737 CACTCCTGGGAACAGAAAGTTTATTGCAAGCGCTCTCTTAGATGAACCTGTTG 1796  
Qy 347 AGTGACACATTTCCGACCATCTACCATGTTTCATCGCTGGCTGTGTCTTCATCA 406  
Db 1797 AAGTGACACATCTACGACCAATATATCATGTTTATGCGCTCTCATCTTTATCC 1856  
Qy 407 TCAGACCTGGCCATCGACTTCTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 466  
Db 1857 TCAGACATCTGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1916  
Qy 467 TGATCTTCGAGCTCGGAGAGCTGCCATTTGGCGCTGGTGACCTGGCCCATGTTCTGT 526  
Db 467 TGATCTTCGAGCTCGGAGAGCTGCCATTTGGCGCTGGTGACCTGGCCCATGTTCTGT 526









QY	922	GTGCTCTATGCCCTGCTCTCATCTCGGGCCGCCCTCTGTGTTCTCTGCTTTTGCCAAACATGAGC	981
Db	2396	TTTTTCTATGTGTACTACATCTTTGAAAGGCTTTGTGCCCTCTGTTTCGGAATATCAAA	2455
QY	982	CGAGAGCCCTTCAGCACCGTCGCCCTGGTGCTCTCTATCTCTGCATGCCACGTTGCCAGGC	1041
Db	2456	CAGAGCCCTTCAGCCGCTCGTGTCTGGTCCATGTGATTTAACTCATCTCCCGCAGGT	2515
QY	1042	ATCTTTCATGCTGCTGCTCATCTTCTTTGGCTTCCCTCCCATTTGCTGTGGCTCAAGCCCTTTTGCC	1101
Db	2516	GTGCTGATTCTCTCCCTTACTTTTTTGGCTTTTGGACTGCTGGCTCAATGGCCTTTGCT	2575
QY	1102	GAGATGCTAGGATTTGGAGACAGAGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTC	1161
Db	2576	GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGTGGAACTCCACGCTCATAC	2635
QY	1162	TCCAACCTACTACCGCACTTTGGAACCTGGTGGTGCCATGACTGSCGTACAGCTACGCTCAT	1221
Db	2636	TCCAACCTATTAGAACCTGGAAATGGTGGTGCCATGACTGGCTATATTACTATGCTTTAC	2695
QY	1222	CAGGATGGGCTGGGCTCCCTTGGTCCCGCCGGCCGAGGGGTAGGCATGCTGGGTGTGTTTC	1281
Db	2696	AAGGACTTTTCTCTGGTTTTTCTCCAAGAGATTCAAATCTGCTGCCATGTTAGCTGCTCTT	2755
QY	1282	CTGGTCTCCGCACTGCCCCATGAGTATATCTTCGTCTCGCTCTGGGGTCTTCTCATCC	1341
Db	2756	GCTGTATCTGCTGTAGTACACAAATGCCTTGGCTGTTGCTTTGAGCTTTTCTATCCC	2815
QY	1342	GTCACTGCTGATACTCTTCCTTCATTCGGAGGAATGTTGAACTTCATGTCATGCATGACCAG	1401
Db	2816	GTGCTGTTTCGTGCTCTTCATGTTCTTTGGAATGGCTTTCACTTTCATGTGCAATGATAGT	2875
QY	1402	CGCACCGGCCCGCATGGAACCTGCTGATGTGGACCATGCTGTGTTTCTAGCGAGGGAATC	1461
Db	2876	CGGAAAAACCCGATTGGAATTTCTGATGTGGACTTCTCTTTTCTTTGGGCAATGGAGTC	2935
QY	1462	CAGGTCAGGCTGTACTGCCAGAGTGTACACGCGGGCACTGCCCTTACCCCCAGGCA	1521
Db	2936	TTACTCTGTTTTTATCTCAAGATGGTATGCATCGGCACTGCTCTTGAAAAATCCC	2995
QY	1522	ACTTTCTGGGGCTGGTGACACCTCGATCTTGGTCCCTGCCAT	1563
Db	2996	ACATTTTTGGATTATGTCCGGCCAGGTTCCCTGGACTGTGCTGT	3037

## RESULT 6

US-08-121-057-2  
; Sequence 2, Application US/08121057  
; Patent No. 5484727  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, TA-YUAN  
; APPLICANT: CHANG, CATHERINE C. Y.  
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,057  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAMPORT HAMMITTE, ANN.



Db 2828 TATCTGCTAGTACAGAAATGCTTGGCTGTGCTTTGCTTTGAGCTTTTCTATCCGCTGC 2887  
QY 1346 TGTGTATACACTCTCTTGTCTATTGAGAGAAATGTTGAACATTCATGATCATGACACGCGCA 1405  
Db 2888 TGTTCGTGCTCTTCTCATGCTTCTTGGATGCTTCAACATTCATGTCATGATAGTCGGA 2947  
QY 1406 CCGGCCCGGATGAGAGCTGCTGATGAGACCATGCTGTTTCAGGCCAGGGAATCCAGG 1465  
Db 2948 AAAAGCCGATTTGGAAATGTTCTGATGAGACTTCTCTTTCTTTGGGCAATGGAGTCTTAC 3007  
QY 1466 TCAGCCTGTACTGCCAGAGTGTACGACGCGGCGCACTCCCT 1510  
Db 3008 TCTGCTTTTATCTCAAGATGGTATGACAGCTGCGCACTGTACCT 3052

## RESULT 8

US-09-121-396-2

; Sequence 2, Application US/09121396

; Patent No. 5968749

; GENERAL INFORMATION:

; APPLICANT: CHANG, TA-YUAN

; APPLICANT: CHANG, CATHERINE C. Y.

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 28 STATE STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/121,396

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/509,187

; FILING DATE: 07/31/95

; ATTORNEY/AGENT INFORMATION:

; NAME: LAMPORT HAMMITTE, ANN.

; REGISTRATION NUMBER: 34,858

; REFERENCE/DOCKET NUMBER: DCI-033CPDV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-2700

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4079 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-121-396-2

Query Match 22.9%; Score 359.8; DB 2; Length 4079;  
Best Local Similarity 58.0%; Pred. No. 6.6e-83;  
Matches 722; Conservative 0; Mismatches 502; Indels 21; Gaps 4;  
QY 287 CATCCCTGGGAAACAGAAAGTTTCATCATCCGAAAGTCCCTGCTGATGAGCTGATGG 346  
Db 1808 CACCTCCAGAAAGAAAGATTTTATTGCAAGGCGCTCTCTCTAGATGAAGTCTTG 1867  
QY 347 AGGTGACGATTTCCGACCATCTACCATGTTCTATCGCTGGCTGTGCTTCATCA 406  
Db 1868 AGTGGACCACATCAGAAATATATACATGTTTATTGCGCTCTCTTATTC 1927

QY 407 TCAGCACCCCTGGCCATCGACTTCATTATGAGGCGCAGGCTGCTGCTGG--AGTTTGACCT 464  
Db 1928 TCAGCACACTTGTAGTAGATTACATTGATGAAGAGGCTGGTGGCTTGAAGTTAGCCCT 1987  
QY 465 ACTG-ATCTTCAGCTTCGACAGCTGCCATGTCGCGTGTGACCTGGTGGTCCCATTTTC 523  
Db 1988 CTTGCTCTTATGCAATTTTGGCAAAATTTCTACCGCTTCTTTGGACCTGGTGGATCATCTTC 2047  
QY 524 TGTCCACCCCTGTTGGCGCGTACACAGCCCTACGCGTGTGGCGGAGGCGACCTTGACGC 583  
Db 2048 TGTCTACATTTTCAGTTCCTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGA 2107  
QY 584 AGCGACGCGGCTGGGCTGTGCGCTTTTAGCGGCCACGCGCTGGTGTCTCTGCGCCTGC 643  
Db 2108 GTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 2167  
QY 644 CGGTCCACGTGGCGG-----TGGAGCATCAGCTCCGCGGCGCTCCCGCTTGT 690  
Db 2168 GAGTTCCTAGGTTTGGACCAACATATGTTGTGTAGCATATCTGCCACAGCTTCCCGG 2227  
QY 691 GTCCTGCTCTCGACGAGGTAGTTCCTGATGAAAGCTACTCTTCTCTCTGAGAGGCT 750  
Db 2228 TTTCACTATTTCGACGACATCGTTTGTGTAAGAGGCCCATCTCATTTGTCAGAGAGAAC 2287  
QY 751 GTGCTGGGATCCTTGTGTCGACAGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
Db 2288 GTGCTCGGCTACTTATTTGCTCTCCACCTTATCTTACCGTGACAGCTATCCAGTCA 2347  
QY 806 CCAGCTACCTCTACTCTCTTCTGCCCCAACACTATCTACAGGAGACTTACCTTAGCA 865  
Db 2348 ACAGTATTGTACTTCTTATTTGCTCTCCACCTTATCTTACCGTGACAGCTATCCAGGA 2407  
QY 866 CGCCCTATCTCAGGTGGAAATATGTTGGCCAAAGAACTTTGCCAGGCGCTTGGATGTGTC 925  
Db 2408 ATCCCACTCTAAGATGGGTTTATGTTGCTATGAAGTTTGCACAGGCTTTTGGTGTCTTT 2467  
QY 926 TCTATGCTGCTCATCTCTGCGCGGCTCTGTGTTCTGCTCTTTTGGCAACATGAGCCGAG 985  
Db 2468 TCTATGTGACTACATCTTTTGAAGGCTTTTGTGCCCGCTTTTGGGAATATCAACAGG 2527  
QY 986 AGCCCTTCAGCACCGCTGCCCTGCTCTCTATCTGATGCCAGTTCGCCAGGCTATCT 1045  
Db 2528 AGCCCTTCAGCGCTGCTGTTCTGCTCTATGTTTAACTTCCATCTTGCAGGCTGTC 2587  
QY 1046 TCATGCTGCTCATCTCTTCTTGTGCTTCTCTCAATGTGCTCAACGCTTTTGGCGAGA 1105  
Db 2588 TGATTTCTCTCTTCTTCTTTTGGCTTTTGTGCTGCTGCTCAATGCTTGTGCTGAGA 2647  
QY 1106 TGTCTAGATTTCGACAGAGATGTTTCTACCGGAGTGTGGGAACTCAAGCTCTTCTCCA 1165  
Db 2648 TGTTAGCTTTGTCGACAGAGATGTTCTATAGGATTTGGTGGAACTCCAGCTCATATCCA 2707  
QY 1166 ACTACTACCGCACTTGGAACTGGTGGTCTCATGCTGCTGTACAGTACGCTGTATCAGG 1225  
Db 2708 ACTATTATAGAACCCTGGAATGTTGTTGCTTCCATGACTGGCTATATTACTATGCTTACAAG 2767  
QY 1226 ATGGGCTGGGCTCCTTGTGCGCGGCGGAGGGGTAGCCATGCTGGGTGTTGCTCTGG 1285  
Db 2768 ACTTTCTCTGTTTCTTCTCAAGAGATTTCAAAATCTGCTGCCATGTTAGTGTCTTTGCTG 2827  
QY 1286 TCTCCGCACTGGCCCATGAGTATATCTTCTGCTCTGCTGGGCTTCTTATATCCGCTCA 1345  
Db 2828 TATCTGCTGTAGTACAGAAATGCTGCTGGCTGTTGCTTGGCTTTTCTATCCCGTGC 2887  
QY 1346 TGTCTGATCTCTTCTGTCATTTGAGGAAATGTTGAACATTCATGATGATGATGACGCGCA 1405  
Db 2888 TGTTCGCTCTCTCATGTTCTTTGGAATGGCTTTTCAACTTCAATGCTCAATGATAGTCGGA 2947  
QY 1406 CCGGCCCGGATGGAACGCTGCTGATGTGGACCATGCTCTTTCTTAGGCGAGGGAATCCAGG 1465  
Db 2948 AAAAGCCGATTTGGAATGTTCTGATGTGGAATGTTCTCTTTTCTTTGGCAATGAGTCTTAC 3007  
QY 1466 TCAGCTGTACTGCCAGGAGTGGTACGACAGGCGCACTGCCCT 1510



COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/121,057  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: LAMPORT HAMMITTE, ANN.  
REGISTRATION NUMBER: 34,858  
REFERENCE/DOCKET NUMBER: DCI-033CP  
TELEPHONE: (617) 227-2700  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 996 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-121-057-1

Query Match 8.6%; Score 134.6; DB 1; Length 996;  
Best Local Similarity 53.1%; Pred. No. 2.6e-25;  
Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

Db 287 CATCCCTGGGGAACAGAAAGTTTCATCATCCGAAAGTCCCTGCTGTATGAGCTGATGG 346  
QY  
Db 262 CACCTCCAGAACAGAAAGATTTTATTGCAAGGGCTCTCTCTTAGACTGCTTGC 321  
QY  
Db 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406  
QY  
Db 322 AGTGGACCATCAGAACATATATACATGTTTATTGCCCTCCTCTCTTTATCC 381  
QY  
Db 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGCGAGGCTGCTGTGG--AGTTGACCT 464  
QY  
Db 382 TCAGCACACTTGTAGTAGATTACATTTGATGAAGGAGGCTGCTGTGAAGTTAGCCT 441  
QY  
Db 465 ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGTGACCTGGTGCCCATCTTTC 523  
QY  
Db 442 CCTGCTTATGCAATTTGGCAAAATTTCTACCTGTTTGGACCTGGTGATCATCTTC 501  
QY  
Db 524 TGTCACCTGTTGGGGCCGTACAGGCCCTACGGCTGTGGCCAGGGCACCTGGACGC 583  
QY  
Db 502 TGCTACATTTTCAGTTCCCTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAG 561  
QY  
Db 584 AGCGAGGGCCCTGGGCTGTGCGCTTTTACGCCGCCACGCCGTGTGCTC-----633  
QY  
Db 562 GTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621  
QY  
Db 634 ---TGGCGCTCGCGTCCAGCTGGCGGTGGAGCATCAGTCCCGCGGCTCCCTGTTG 690  
QY  
Db 622 GAGTTCTAGTGTGGACCAACATATGTTGTGTAGCATATCTGCTGACATCTGCTCCCG 681  
QY  
Db 691 GTCTGTGCTTCGAGCAGGTTAGTTCCTGATGAAAGCTACTCCTCTCTGAGAGGCT 750  
QY  
Db 682 TTATCATATTTCGAGCAGATCGTTTGTGAAGAGGCCACTCAATTTGTCAGAGAGAAC 741  
QY  
Db 751 GTGCTGGGATCCTTGTGCGACAGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
QY  
Db 742 GTGCTGGGTACTAATTCAGTAAGAGANAATCAGCACTGTTCATACCTACAGTCA 801  
QY  
Db 806 CCAGCTACCTCTACTTCTCTCTGCCCCAACACTATCTACAGGAGACTTACCTTAGGA 865  
QY  
Db 802 ACCAGTATTTGACTTCTTATTTGCTTCTTACCTTATCTACCGTGACAGTATCCAGGA 861  
QY  
Db 866 CGCCCTATGTCAGGTGAATTTGTGCCNAGAACATTTGCCAGGCCCTGGGATGTGTC 925  
QY

Db 862 ATCCCACTGTAAGATGGGCTTATGTTGCTATGAAGTTCCACAGGCTTTGGTGTCTTT 921  
QY  
Db 926 TCTATGCTGCTTCATCTCGGCGGCTCTGTGTTCTCTCTTTGCAACATGAGCCGAG 985  
QY  
Db 922 TCTATGCTGCTACATCTTTGAAGGCTTTGTGCCCCCTTTGTTGGATATACAAACAG 981  
QY  
Db 986 AGCCCTTCAGCACCC 1000  
QY  
Db 982 AGCCCTTCAGCGCTC 996

RESULT 11  
US-08-509-187D-1  
; Sequence 1, Application US/08509187D  
; Patent No. 5834283  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.  
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/509,187D  
; FILING DATE: 31-JUL-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lamport Hammitte, Ann  
; REGISTRATION NUMBER: 34,858  
; REFERENCE/DOCKET NUMBER: DCI-033cpdv  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 996 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-509-187D-1

Query Match 8.6%; Score 134.6; DB 2; Length 996;  
Best Local Similarity 53.1%; Pred. No. 2.6e-25;  
Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACAGAAAGTTTCATCATCCGAAAGTCCCTGCTGTATGAGCTGATGG 346  
Db 262 CACCTCCAGAACAGAAAGATTTTATTGCAAGGGCTCTCTCTTAGACTGCTTGC 321  
QY 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406  
Db 322 AGTGGACCATCAGAACATATATACATGTTTATTGCCCTCCTCTCTTTATCC 381  
QY 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGCGAGGCTGCTGTGG--AGTTGACCT 464  
Db 382 TCAGCACACTTGTAGTAGATTACATTTGATGAAGGAGGCTGCTGTGAAGTTAGCCT 441  
QY 465 ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGTGACCTGGTGCCCATCTTTC 523  
Db 442 CCTGCTTATGCAATTTGGCAAAATTTCTACCTGTTTGGACCTGGTGATCATCTTC 501  
QY 524 TGTCACCTGTTGGGGCCGTACAGGCCCTACGGCTGTGGCCAGGGCACCTGGACGC 583  
Db 502 TGCTACATTTTCAGTTCCCTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAG 561  
QY 584 AGCGAGGGCCCTGGGCTGTGCGCTTTTACGCCGCCACGCCGTGTGCTC-----633  
Db 562 GTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621  
QY 634 ---TGGCGCTCGCGTCCAGCTGGCGGTGGAGCATCAGTCCCGCGGCTCCCTGTTG 690  
Db 622 GAGTTCTAGTGTGGACCAACATATGTTGTGTAGCATATCTGCTGACATCTGCTCCCG 681  
QY 691 GTCTGTGCTTCGAGCAGGTTAGTTCCTGATGAAAGCTACTCCTCTCTGAGAGGCT 750  
Db 682 TTATCATATTTCGAGCAGATCGTTTGTGAAGAGGCCACTCAATTTGTCAGAGAGAAC 741  
QY 751 GTGCTGGGATCCTTGTGCGACAGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
Db 742 GTGCTGGGTACTAATTCAGTAAGAGANAATCAGCACTGTTCATACCTACAGTCA 801  
QY 806 CCAGCTACCTCTACTTCTCTCTGCCCCAACACTATCTACAGGAGACTTACCTTAGGA 865  
Db 802 ACCAGTATTTGACTTCTTATTTGCTTCTTACCTTATCTACCGTGACAGTATCCAGGA 861  
QY 866 CGCCCTATGTCAGGTGAATTTGTGCCNAGAACATTTGCCAGGCCCTGGGATGTGTC 925  
Db







RESULT 15  
US-09-165-042-2  
; Sequence 2, Application US/09165042  
; Patent No. 6100077  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331  
; CURRENT APPLICATION NUMBER: US/09/165,042  
; CURRENT FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1976  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-165-042-2

Query Match 6.1%; Score 95; DB 3; Length 1976;  
Best Local Similarity 58.7%; Pred. No. 5e-15;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
  
QY 1019 TCCTGCATGCCAGCTGCCAGGATCTTCATGCTGCTCATCTTTGCCCTTCCTCC 1078  
Db 1212 TCCTGAAGCTGGGGTCCCAATCACCTCATCTGGCTCATCTTCTACTGGCTCTCC 1271  
  
QY 1079 ATTGCTGGCTCAAGCCCTTTGCCGAGATGCTACGATTTGGAGACAGATGTTCTACCGG 1138  
Db 1272 ACTCCTGCCTGAATGCCGTGGCTGAGCTCATGCACTTTGGAGACCGGGAGTTCTACCGG 1331  
  
QY 1139 ACTGGTGAACCTCAACGTCTCTTCCAACTACTACCCGACTTGAACGCTGGTGGTCCATG 1198  
Db 1332 ACTGGTGAACCTCGAGTCTGTCACTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 1391  
  
QY 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGCTCGGGCTCTTGGTGCCCGGCCCGAG 1258  
Db 1392 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1445  
  
QY 1259 GGTAGCCATGCTGGGTGTGTTCTGCTCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 1446 GGATGGCCAGGACAGGGGTGTCTGCTCCCTCGGCTTTCTTCCACGAGTACCTGGTGAGCG 1505  
  
QY 1319 TCGTCCTGGGTTCTTC 1335  
Db 1506 TCCCTCTGCGAATGTTTC 1522

Search completed: April 28, 2003, 16:12:43  
Job time : 112 secs

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GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 06:12:58 ; Search time 113 seconds  
(without alignments)  
15108.619 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggagccaggcgggcccg.....cttggctcgcatacctag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published\_Applications\_NA.\*
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PTCT\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
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  - 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	403.6	25.7	418	9	US-09-918-995-33158
2	391	24.9	399	9	US-09-918-995-33281
3	387.2	24.7	401	9	US-09-918-995-33355
4	386	24.6	402	9	US-09-918-995-33444
5	385.6	24.6	401	9	US-09-918-995-33843
6	384	24.5	393	9	US-09-918-995-33739
7	376.2	24.0	401	9	US-09-918-995-33159
8	350.6	22.3	365	9	US-09-918-995-34424
9	350.6	22.3	408	9	US-09-918-995-34099
10	338.2	21.6	383	9	US-09-918-995-35056
11	138.8	8.8	471	9	US-09-918-995-33288
12	95	6.1	993	10	US-09-764-853-79
13	95	6.1	1411	9	US-10-273-438-1
14	95	6.1	1895	9	US-10-157-855-14
15	93.8	6.0	542	9	US-09-764-868-587
16	92.4	5.9	774	9	US-09-764-868-279
17	81.4	5.2	447	9	US-09-918-995-23256
18	81.4	5.2	452	10	US-09-867-701-4664
19	81.4	5.2	1650	9	US-10-273-438-3

20	81.4	5.2	1650	9	US-10-273-438-9	Sequence 9, Appli
21	80	5.1	1122	9	US-09-774-639-29	Sequence 29, Appli
22	80	5.1	1122	9	US-09-969-730-58	Sequence 58, Appli
23	79.8	5.1	1766	9	US-10-157-855-15	Sequence 15, Appli
24	79.8	5.1	1766	9	US-10-157-855-16	Sequence 16, Appli
25	70.2	4.5	1572	9	US-10-223-076-17	Sequence 17, Appli
26	67.6	4.3	1181	9	US-10-223-076-16	Sequence 16, Appli
27	57.8	3.7	2099	9	US-10-223-076-12	Sequence 12, Appli
28	55.4	3.5	519	9	US-10-157-855-11	Sequence 11, Appli
29	54.2	3.5	471	9	US-09-918-995-1979	Sequence 1979, Ap
30	53.6	3.4	1964	9	US-10-223-076-14	Sequence 14, Appli
31	52.6	3.4	1537	9	US-10-223-076-4	Sequence 4, Appli
32	52.4	3.3	1446	9	US-10-223-076-6	Sequence 6, Appli
33	52.4	3.3	1512	9	US-10-223-076-8	Sequence 8, Appli
34	50	3.2	1904	9	US-10-223-076-2	Sequence 2, Appli
35	50	3.2	1942	9	US-10-157-855-1	Sequence 1, Appli
36	49	3.1	2090	9	US-10-223-076-10	Sequence 10, Appli
37	47.8	3.0	380	10	US-09-770-791-192	Sequence 192, App
38	45.8	2.9	433	10	US-09-764-853-314	Sequence 314, App
39	43.8	2.8	275	10	US-09-878-574-15694	Sequence 15694, A
40	41.8	2.7	790	9	US-10-123-155-204	Sequence 204, App
41	41.8	2.7	2802	10	US-09-815-242-7720	Sequence 7720, Ap
42	41.2	2.6	2715	9	US-09-712-363-101	Sequence 101, App
43	40.6	2.6	594	9	US-10-123-155-10	Sequence 10, Appli
44	40.6	2.6	1089	10	US-09-866-562-60	Sequence 60, Appli
45	40.6	2.6	1176	10	US-09-866-562-59	Sequence 59, Appli

ALIGNMENTS

RESULT 1

US-09-918-995-33158  
; Sequence 33158, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33158  
; LENGTH: 418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-33158

Query Match	25.7%	Score	403.6	DB	9	Length	418
Best Local Similarity	99.0%	Pred. No.	3.4e-110				
Matches	406	Conservative	0	Mismatches	4	Indels	0
Gaps	0						
QY	1122	CAGGATGTTCTACGGGACTGGTGAACCTCAAGCTCTCTCCAACTACTACGCACTTG	1181				
Db	9	CAGGATGTTCTACGGGACTGGTGAACCTCAAGCTCTCTCCAACTACTACGCACTTG	68				
QY	1182	GAACGTTGGTGGTCCATGACTGGCTGTACAGTACGTGTATCAGATGGGTGGCGTCTCT	1241				
Db	69	GAACGTTGGTGGTCCATGACTGGCTGTACAGTACGTGTATCAGATGGGTGGCGTCTCT	128				
QY	1242	TGTTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCTGCTCCCGAGTGGCCCA	1301				
Db	129	TGTTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCTGCTCCCGAGTGGCCCA	188				
QY	1302	TGAGTATATCTTCTGCTCTCTCTCTGCGGTTCCTTCTATCCGCTGATGCTACTTCTCT	1361				
Db	189	TGAGTATATCTTCTGCTCTCTCTCTGCGGTTCCTTCTATCCGCTGATGCTACTTCTCT	248				
QY	1362	TGTCATTGGAGGAATGTTGAACCTTCATGATGCATGACACCGACCGCCCGCATGAA	1421				

Db 249 TGTCATTGGAGGAATTTGAACCTTCATGATGACACGAGCAGCCGCGCGCATGGAA 308  
QY 1422 CGTGCTGATGTGGACCATCTGTTTACGCCAGGGAATCCAGGTACAGCTGTACTGCCA 1481  
Db 309 CGTGCTGATGTGGACCATCTGTTTACGCCAGGGAATCCAGGTACAGCTGTACTGCCA 368  
QY 1482 GGAGTGGTACGACGCGGCACTGCCCTTACCCAGGCAACTTTCTGGG 1531  
Db 369 GGAGTGGTACGACGCGGCACTTGCCCTTACCCAGCAACTTCTGGG 418

## RESULT 2

US-09-918-995-33281  
; Sequence 33281, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33281

; LENGTH: 399

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-33281

Query Match 24.9%; Score 391; DB 9; Length 399;

Best Local Similarity 100.0%; Pred. No. 1.9e-106; Indels 0; Gaps 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181

Db 9 CAGGATGTTCTACCGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACCTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGGATGGGCTCGGCTCCT 1241

Db 69 GAACCTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGGATGGGCTCGGCTCCT 128

QY 1242 TGGTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCCGCACTGGCCCA 1301

Db 129 TGGTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCCGCACTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCCTCGGGTTCCTTATCCCGTCACTGATCTCTTCT 1361

Db 189 TGAGTATATCTTCTGCTTCCTCGGGTTCCTTATCCCGTCACTGATCTCTTCT 248

QY 1362 TGTCATTGGAGGAATGTTGAACCTTCATGATGACACGAGCAGCGCCGCGCATGGAA 1421

Db 249 TGTCATTGGAGGAATGTTGAACCTTCATGATGACACGAGCAGCGCCGCGCATGGAA 308

QY 1422 CGTGCTGATGTGGACCATCTGTTTCTAGCCAGGGAATCCAGGTACAGCTGTACTGCCA 1481

Db 309 CGTGCTGATGTGGACCATCTGTTTCTAGCCAGGGAATCCAGGTACAGCTGTACTGCCA 368

QY 1482 GGAGTGGTACGACGCGGCACTTGCCCTTACCCAGCAACTTCTGGG 1512

Db 369 GGAGTGGTACGACGCGGCACTTGCCCTTACCCAGCAACTTCTGGG 399

## RESULT 3

US-09-918-995-33355  
; Sequence 33355, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33355

; LENGTH: 401

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(401)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-33355

Query Match 24.7%; Score 387.2; DB 9; Length 401;

Best Local Similarity 99.0%; Pred. No. 2.5e-105;

Matches 389; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181

Db 9 CAGGATGTTCTACCGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACCTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGGATGGGCTCGGCTCCT 1241

Db 69 GAACCTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGGATGGGCTCGGCTCCT 128

QY 1242 TGGTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCCGCACTGGCCCA 1301

Db 129 TGGTGCCGCGGCGGAGGGTAGCCATGCTGGGTGTTCTTCCGCACTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCCTCGGGTTCCTTATCCCGTCACTGATCTCTTCT 1361

Db 189 TGAGTATATCTTCTGCTTCCTCGGGTTCCTTATCCCGTCACTGATCTCTTCT 248

QY 1362 TGTCATTGGAGGAATGTTGAACCTTCATGATGACACGAGCAGCGCCGCGCATGGAA 1421

Db 249 TGTCATTGGAGGAATGTTGAACCTTCATGATGACACGAGCAGCGCCGCGCATGGAA 308

QY 1422 CGTGCTGATGTGGACCATCTGTTTCTAGCCAGGGAATCCAGGTACAGCTGTACTGCCA 1481

Db 309 CGTGCTGATGTGGACCATCTGTTTCTAGCCAGGGAATCCAGGTACAGCTGTACTGCCA 368

QY 1482 GGAGTGGTACGACGCGGCACTTGCCCTTACC 1514

Db 369 NGAGTGGTACGACGCGGCACTTGCCCTTACC 401

## RESULT 4

US-09-918-995-33444

; Sequence 33444, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 33444

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-33444

Query Match 24.6%; Score 386; DB 9; Length 402;

Best Local Similarity 98.7%; Pred. No. 5.8e-105;  
Matches 389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCCGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTGTCCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCCGGCCGAGGGGTAAACATGCTGGGTGTGTTCTGTCCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACCGCGGCGCACTGCCCTTACC 1515  
Db 369 GGAGTGGTACCGCGGCGCACTGCCCTTACC 402

RESULT 5  
US-09-918-995-33843  
; Sequence 33843, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33843  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-918-995-33843

Query Match 24.6%; Score 385.6; DB 9; Length 401;  
Best Local Similarity 99.0%; Pred. No. 7.6e-105;  
Matches 388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCCGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTGTCCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCCGGCCGAGGGGAACCATGCTGGGTGTGTTCTGTCCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACCGCGGCGCACTGCCCTTACC 1513  
Db 369 GGAGTGGTACCGCGGCGCACTGCCCTTACC 400

RESULT 6  
US-09-918-995-33739  
; Sequence 33739, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33739  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(393)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-33739

Query Match 24.5%; Score 384; DB 9; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.3e-104;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCCGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTGCTCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCCGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTGCTCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCTGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACCGCGGCGCACTG 1505  
Db 369 GGAGTGGTACCGCGGCGCACTG 392

RESULT 7  
US-09-918-995-33159





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QY 1362 TGTCAATGGAGGATGTTGAACCTTCATGATGACGACGACCGCCGCGGATGAA 1421
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Db 255 TGTCAATGGAGGATGTTGAACCTTCATGATGACGACGACCGCCGCGGATGAA 314
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; Sequence 35056, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35056
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(383)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35056
Query Match 21.6%; Score 338.2; DB 9; Length 383;
Best Local Similarity 95.1%; Pred. No. 9.7e-91;
Matches 349; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGACCTGGTGGAACTCAACGCTCTCTCCAACTACTACCGCACTTG 1181
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Db 9 CAGGATGTTCTACCGGACCTGGTGGAACTCAACGCTCTCTCCAACTACTACCGCACTTG 68
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QY 1182 GAACGTGGTGGTCCATGACTGCTGTACAGCTAGCTATCAGGATGGGCTGCGGCTCCT 1241
|||||
Db 69 GAACGTGGTGGTCCATGACTGCTGTACAGCTATCAGGATGGGCTGCGGATCCT 128
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QY 1242 TGGTCCCGGCGGCGAGGGTAGCATGCTGGGTGTCTCTGCTCCGAGTGCGCCA 1301
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Db 129 TGGTCCCGGCGGCGAGGGTAGCATGCTGGGTGTCTCTGCTCCGAGTGCGCCA 188
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QY 1302 TGAGTATATCTTCGCTTCGCTCGGCGGTTCTTATCCCGTATGCTGATCTTCCT 1361
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Db 189 TGAGTATATCTTCGCTTCGCTCGGCGGTTCTTATCCCGGATGCTGATCTTCCT 248
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QY 1362 TGTCAATGGAGGATGTTGAACCTTCATGATGACGACGACCGCCGCGGATGAA 1421
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Db 249 TGTCAATGGAGGATGTTGAACCTTCATGATGACGACGACCGCCGCGGATGAA 308
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QY 1422 CGTGTGATGTGGACCATGCTGTTTCTAGGCGAGGAATCCAGGTGAGCTGTACTGCCA 1481
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Db 309 CGTGTGATGTGGACCATGCTGTTTCTAGGCGAGGAATCCAGGTGAGCTGTACTGCCA 368
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QY 1482 GGAGTGG 1488
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Db 369 CGAGTGG 375
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US-09-918-995-32388
; Sequence 32388, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32388
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32388
Query Match 8.8%; Score 138.8; DB 9; Length 471;
Best Local Similarity 92.4%; Pred. No. 2.4e-31;
Matches 146; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 943 CTGGCGCGCTCTCTGTTCCTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 1002
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Db 228 CTGGCGCGCTCTCTGTTCCTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 287
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RESULT 12
US-09-764-853-79/c
; Sequence 79, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-79
Query Match 6.1%; Score 95; DB 10; Length 993;
Best Local Similarity 58.7%; Pred. No. 3.6e-18;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTCTCTTTCCTCTCC 1078
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QY 1079 ATTGCTGGCTCAACGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTGTACCGGG 1138
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Db 720 ACTCTGCTGAATGCCGCTGAGCTCATGCGAGTTTGGAGACCGGGAGTTCTACCGGG 661
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QY 1139 ACTGTGGAACCTCAACGCTCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198
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Db 660 ACTGGTGAACCTCGAGTCTGTACCTTCTGGCAGAACTGGAACATCCCTGTGCACA 601  
QY 1199 ACTGGCTGTACAGCTAGCTATCAGATGGCTCGGCTCTTGTGGTCCGCCGCCGAG 1258  
Db 600 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 547  
QY 1259 GGGTAGCCATGCTGGGTGTGTTCTGTCTCCGAGTGGCCCATGAGTATATCTTCGCT 1318  
Db 546 GGATGGCCAGACAGGGGTGTTCTGTGCTCGGCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 487  
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Db 486 TCCCTCTGCGAATGTTTC 470  
RESULT 13  
US-10-273-438-1  
; Sequence 1, Application US/10273438  
; Publication No. US20030072757A1  
; GENERAL INFORMATION:  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Smith, Steven  
; APPLICANT: Erickson, Sandra  
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase  
; FILE REFERENCE: UCAL-105C1F2  
; CURRENT APPLICATION NUMBER: US/10/273,438  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US/10/040,315  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/107,771  
; PRIOR FILING DATE: 1998-11-09  
; PRIOR APPLICATION NUMBER: PCT/US98/17883  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 09/103,754  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 09/339,472  
; PRIOR FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-273-438-1  
Query Match 6.1%; Score 95; DB 9; Length 1411;  
Best Local Similarity 58.7%; Pred. No. 4.1e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
QY 1019 TCCTGCATGCCAGCTTGGCCAGGCATCTTCATGCTGTGCTCATCTTCTTGTGCTTCTCTCC 1078  
Db 662 TCCTGAAGCTGGGGTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTTCTCC 721  
QY 1079 ATTGCTGGCTCAACGCTTTCGGGAGATGCTAGATTTGGACAGAGATGTTCTACCCGG 1138  
Db 722 ACTCTTCCTGATGCGGTGGTGGTCTCATGAGTTTGGAGACCGGGAGTTCTACCCGG 781  
QY 1139 ACTGGTGAACCTCAAGCTCTTCTTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198  
Db 782 ACTGGTGAACCTCCGAGTCTGTACACTTCTTGGCAGAACTGGAACATCCCTGTGCACA 841  
QY 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGTGGGCTGCTTGTGTCGCCGCCGAG 1258  
Db 842 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 895  
QY 1259 GGGTAGCCATGCTGGGTGTGTTCTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 896 GGATGCCAGGACAGGGGTGTTCTGTGCTCGGCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 955  
QY 1319 TCGTCTCGGGTCTTTC 1335  
Db 1199 TCGTCTCGGGTCTTTC 1335  
Db 1207 TCCCTCTGCGAATGTTTC 1223  
RESULT 15  
US-09-764-868-587  
; Sequence 587, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper

Db 956 TCCCTCTGCGAATGTTTC 972  
RESULT 14  
US-10-157-855-14  
; Sequence 14, Application US/10157855  
; Patent No. US20020170091A1  
; GENERAL INFORMATION:  
; APPLICANT: Lassner, Michael W.  
; APPLICANT: Ruezinsky, Diane M.  
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic  
; TITLE OF INVENTION: Acid Sequences  
; FILE REFERENCE: 16516.158  
; CURRENT APPLICATION NUMBER: US/10/157,855  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: 09/326,203  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 60/088,143  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/108,389  
; PRIOR FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1895  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (209)  
; OTHER INFORMATION: n at position 209 is unknown  
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Query Match 6.1%; Score 95; DB 9; Length 1895;  
Best Local Similarity 58.7%; Pred. No. 4.6e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
QY 1019 TCCTGCATGCCAGCTTGGCCAGGCATCTTCATGCTGTGCTCATCTTCTTGTGCTTCTCTCC 1078  
Db 913 TCCTGAAGCTGGGGTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTTCTCC 972  
QY 1079 ATTGCTGGCTCAACGCTTTCGGGAGATGCTAGGATTTGGACAGAGATGTTCTACCCGG 1138  
Db 973 ACTCTTCCTGATGCGGTGGTGGTCTCATGAGTTTGGAGACCGGGAGTTCTACCCGG 1032  
QY 1139 ACTGGTGAACCTCAACGCTCTTCTTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198  
Db 1033 ACTGGTGAACCTCCGAGTCTGTACACTTCTTGGCAGAACTGGAACATCCCTGTGCACA 1092  
QY 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGTGGGCTGCTTGTGTCGCCGCCGAG 1258  
Db 1093 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1146  
QY 1259 GGGTAGCCATGCTGGGTGTGTTCTGTGCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
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QY 1319 TCGTCTCGGGTCTTTC 1335  
Db 1207 TCCCTCTGCGAATGTTTC 1223  
RESULT 15  
US-09-764-868-587  
; Sequence 587, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper



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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 04:51:57 ; Search time 1603 seconds

(without alignments)  
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Title: US-09-918-026a-3

Perfect score: 1569

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	298.2	19.0	778	13	BG920709 602824607
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22	204.2	13.0	553	10	BE013288	BE013288 123187 MA
23	202	12.9	878	14	BQ887458	BQ887458 AGENCOURT
24	200.2	12.8	608	9	AA867781	AA867781 vx16e09.r
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26	186.2	11.9	601	14	BQ200762	BQ200762 UI-R-EB1-
27	185.2	11.8	915	12	BF968277	BF968277 602269663
28	183	11.7	460	14	R10272	R10272 yf36b09.r1
29	181.2	11.5	876	12	BF578775	BF578775 602094805
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31	175	11.2	376	10	AW425878	AW425878 58867 MAR
32	171.8	10.9	655	10	BE026601	BE026601 db28h02.x
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#### ALIGNMENTS

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DEFINITION	mRNA sequence.				
ACCESSION	BI222037				
VERSION	BI222037.1				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 799)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L1AM11238 row: b column: 24 High quality sequence start: 28 High quality sequence stop: 798.				
FEATURES	Location/Qualifiers				





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Best Local Similarity 64.2%; Pred. No. 3.1e-55;
Matches 439; Conservative 0; Mismatches 244; Indels 1; Gaps 1;
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QY 963 TGTCTTGGCAACATGAGCGGAGAGCCCTTACGACCCGCTGCCCTGCTCTCTATCCT 1022
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EST 01-MAY-2001
ACCESSION BG674469
VERSION BG674469.1 GI:13905865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 992)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10593 row: n column: 22

High quality sequence stop: 828.

location/Qualifiers

FEATURES

source

1. .992

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4746069"

/clone\_lib="NCI\_CGAP\_Skn3"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 199 a 216 c 231 g 346 t

ORIGIN

Query Match 17.4%; Score 272.6; DB 12; Length 992;

Best Local Similarity 63.2%; Pred. No. 4.6e-53;

Matches 419; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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QY 961 CCGTCTTTTCCAAACATGAGCGGAGAGCCCTTACGACCCGCTGCCCTGTGCTCTATC 1020

DB 62 CCGTCTTTTCCGAATATCAACAGGAGCCCTTACGCGCTGTCTGCTCTATGTA 121

QY 1021 CTGCATGCCAGCTTGCAGGATCTTCTATGCTGCTCTCATCTTCTTGCCTTCTCCAT 1080

DB 122 TTTAACTCCATCTTGCAGGCTGTGATCTCTTCTTACTTTTTTGCCTTTTGCAC 181

QY 1081 TCGTGTCTCAAGCCCTTTCGCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAC 1140

DB 182 TCGTGTCTCAAGCCCTTTCGCGAGATGCTACGATTTGGAGACAGGATGTTCTATAAGAT 241

QY 1141 TGGTGGAACTCAAGCTCTTCTCCAACTATCCGCACTTGGAACTGGTGTGCTCAATGAC 1200

DB 242 TGGTGGAACTCCAGCTCACTCCAACTATTATAGAACTGGAATGTGTGCTCCATGAC 301

QY 1201 TGGCTGTACAGTACGTGTATCAGGATGGCTGGGCTGCTTGGTCCCGGCCCGGAGG 1260

DB 302 TGGCTATATTACTGCTTTACAAGGACTTTCTCTGGTTTTTCTCCAAGAGATTCAAATCT 361

QY 1261 GTAGGCATGCTGGGTGTGTTCTGCTCCGAGTGGCCCATGATATATCTTCTGCTTC 1320

DB 362 GCTGCCATGTTAGCTGTCTTCTGCTGTATCTGTAGTACAGAAATATGCCCTTGGCTGT 421

QY 1321 GTCTCTGGGTCTTCTATCCCGTCTATGCTGATCTTCTTCTCATTTGAGGAATGTTG 1380

DB 422 TCGTTGAGCTTTTCTATCCCGTCTCTTCGCTCTTCTCATCTTCTTGAATGGCTTTC 481

QY 1381 AACTTCATGATGATGACAGCGCACCGCCCGGATGGAACGTCGTGTATGTGGACCATG 1440

DB 482 AACTTCATGTCATGATGTCGGAAGGCGGATTTGGAATGTTCTGTATGTGGACTTCT 541

QY 1441 CTTGTTTAGCGCAGGGAATCCAGGTCAGCTGACTGTCAGGAGTGGTACACGCGCGG 1500

DB 542 CTTTCTTGGGCAATGGAGTCTTACTCTCTTTATTTCTCAAGAAATGGTATGACGCTCAG 601

QY 1501 CACTGCCCTTACCOCAGGCAACTTTTCTGGGCTGGTGACACCTCGATCTTGGTCTCTGC 1560

DB 602 CACTGCTCTCTGAAAAATCCCACTTTTGGATATGTGCCGCCACGCTTCTCTGGACTTCT 661

QY 1561 CAT 1563



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Db 662 CGT 664

RESULT 6
BG529751
DEFINITION BG529751 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5',
            mRNA sequence.
            linear EST 03-APR-2001
ACCESSION BG529751
VERSION BG529751.1 GI:13521288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 840)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: rgs@nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CMI529 row: k column: 05
            High quality sequence stop: 764.
            Location/Qualifiers
                1..840
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4698748"
                /clone_lib="NIH_MGC_61"
                /tissue_type="embryonal carcinoma"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                Sf11 (99ccctatgccc); Site_2: Sf11 (99ccctatgccc);
                Double-stranded cDNA was prepared from cell line RNA. 5'
                and 3' adaptors were used in cloning as follows: 5'
                adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTAGCGCGGCGGCGACATG-dT(30)BN-3'
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                contained inserts by PCR. This library was enriched for
                full-length clones and was constructed by Clontech
                Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                Library."
                BASE COUNT 163 a 195 c 178 g 304 t
                ORIGIN

Query Match 17.1%; Score 268; DB 12; Length 840;
Best Local Similarity 63.4%; Pred. No. 5.1e-52;
Matches 460; Conservative 0; Mismatches 260; Indels 6; Gaps 3;

Qy 811 TACCTCTACTTCCTCTGCGCCAACTGATCTACAGGAGACTTACCCTAGGAGGCC 870
Db 12 TATTGTACTTCTTATTTGCTTCTACCTTATCTACCGTGACAGCTATCCAGGAATCCC 71
Qy 871 TATGTACGTGGAATATATGTGGCAAGAACTTTCGCCAGGCCCTGGGATGTGCTCTAT 930
Db 72 ACTGTAAGATGGGTATGTGCTATGAAGTTTGACAGGCTCTTGGTGTCTTTCTAT 131
Qy 931 GCCTGCTTCACTTCRGGGCGCCTCTGTGTTCTCTGTTTCCAACTAGAGCGGAGGCC 990
Db 132 GTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTTTTCGGAATATCAACAGAGGCC 191
Qy 991 TTCAGCACCCGTGGCGTGTCTCTATCTGATGCCAGCTTGCAGGAGCATCTTATG 1050
Db 192 TTCAGCGCTGCTGCTGCTATGTGTATTTAACTCCATCTTGCAGGTGCTGATT 251

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Qy 1051 CTGCTGCTCA-TCTCTTTTGGCTTCTCCATTGCTGGCTCAAGCGCTTTGCGGAGATGCT 1109
Db 252 CTCTTCTTACTTTTGGCTTCTCCATTGCTGGCTCAATGCTTTGCTTGAGATGTT 311
Qy 1110 ACGATTTGGAGACGAGATGTTCTACCGGAGCTGGTGGAACTCAACGCTCTCTTCCAAC 1169
Db 312 ACGCTTTGGTACGAGATGTTCTATAAGGATTTGGTGGAACTCCAGCTCATCTCCAAC 371
Qy 1170 CTACCGCACCTTGGACGCTGGTGGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGG 1229
Db 372 TTATAGAACCTGGAATGTTGGTGGTCCATGACTGGCTATATTACTATGCTTCAAGGACTT 431
Qy 1230 GCTCGGCTCTCTGCTGGCCCGGCGGAGGAGTACGCTGGTGGTGGTCTCTCTGCTCTC 1289
Db 432 TCTCTGGTTTTCTCCAAAGATTCAAATCTGCTGCCATGTTAGCTGCTTTGCTGTATC 491
Qy 1290 CGCAGTGGCCCATGAGTATATCTTCTGCTGCTGGTGGTGGTCTTCTATCCCGTCACTG 1349
Db 492 TGTCTAGTACACGAATATGCTTGGCTGTTGCTTGGTGGTCTTCTATCCCGTCTCTT 551
Qy 1350 GATACTCTTCTCTGCTGAGGAGTCTTGAATTCATGATGATGATGATGATGATGATGATG 1408
Db 552 CGTCTCTCTCAATGTTCTTGGAAATGGCTTCAACCTCATGTTCAATGATGATGATGATG 611
Qy 1409 GCCCGCATGGAACCTGCTGATGAGGACCATGCTCTTCTAGGCCAGGAA-TCCAG 1464
Db 612 ACCGATTTGGAATGCTGATGAGGACTTCTCTTTCTTGGCAATGGGAGTCTTACCT 671
Qy 1465 GTCAGCCTGTACTGCCAGGAGTGTGATGACGAGGCGGACTGCCCTTACCAGGACACT 1524
Db 672 CTGCTTTTATTTCTCACGAATGGTATGACGCTGACGCTGCTCTCTGAAAAATCCCA 731
Qy 1525 TTTCTGG 1530
Db 732 TTTTGG 737

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RESULT 7
LOCUS AL527439 893 bp mRNA linear EST 13-FEB-2001
DEFINITION AL527439 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC021YJ22 5
prime, mRNA sequence.
ACCESSION AL527439
VERSION AL527439.1 GI:12790932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 893)
REFERENCE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
                1..893
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="CS0DC021YJ22"
                /clone_lib="LTI_NFL003_NBC3"
                /sex="male"
                /tissue_type="neuroblastoma cells"
                /lab_host="DH10B"
                /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                was primed with a NotI-oligo(dT) primer. Five prime end
                enriched, double-stranded cDNA was digested with Not I and
                cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                vector. Library was normalized. Library was constructed
                by Life Technologies. Contact : Feng Liang Life

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182 TGGTGACAGGATGTTTATAGGAGCTGGTGAACCTTACATCATCTCCAACTACTACAG 241
1176 CACTTGAACGTGTGTGCTCATGACTGGCTGCTACAGTACGTGTATCAGATGGCGCTGG 1235
242 GACCTGGAACGTGTGTGCTGACGACTGGCTGCTACTATATGTTTACAAAGACCTGCTG 301
1236 GCTCTTGGTGGCCGGCCGGAGGGGTAGCCATGCTGGGTGTGTCTCTGCTCCGCGAGT 1295
302 GTTTTCTCGAAGAGGTTCAAACTCGCGCCATGCTGGCGCTCTCGCCCTGCGGCTGT 361
1296 GGCCCATGAGATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1355
362 GGTGACGAGTATGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
1356 CTTCTTGTCTATGAGGAGATGTTGAATCTCATGATCATGATGATGATGATGATGATGAT 1415
422 CTTCTGCTTCTTGAAGGCTTTTAACTTCAATGTTAAAGACAGTCCGAAAGGCCAAT 481
1416 ATGGAAGCTGCTGATGTGGACCATGCTGTTTCTAGGCGAGGGAATCAGGTCAGCCTGTA 1475
482 CTCGAACATCAGGCTTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
1476 CTGCGAGAGTGTACGAGCGGCGACTGCCCCCTTACCCAGGCACTTTCTGG 1530
542 GTCTCAAGAGTGTATGCCCGCAGCACTGTCATCTGAAGAAACCTACATTTCTGG 596

RESULT 9
BG696168 741 bp mRNA linear EST 07-MAY-2001
LOCUS 602659280F1 NC1_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802563 5'
DEFINITION mRNA sequence.
ACCESSION BG696168
VERSION BG696168.1 GI:13961039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10696 row: p column: 20
High quality sequence start: 5
High quality sequence stop: 738.
Location/Qualifiers
1. 741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4802563"
/lab_host="NCI_CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-SPOK6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 140 a 160 c 163 g 278 t
ORIGIN
Query Match 15.68; Score 245; DB 12; Length 741;
Best Local Similarity 63.94; Pred. No. 1.2e-46;
Matches 402; Conservative 0; Mismatches 225; Indels 2; Gaps 2;

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QY 902 TTGCCAGGCCCTGGGATGTGCTCTATGCTCTCTCATCTCGCGCCCTGTGTTC 961
DB 13 TTGCACAGGCTTTGGTGTGCTTTTCTATGTGTAATCATCTTTGAAGAGCT-TGTGCC. 71
QY 962 CTGTCTTTGGCAACATGAGCGAGAGCCCTTTCAGACACCCGCTGCTGTCTCTATCC 1021
DB 72 CTTTGTTCGGAATATCAAAACAGGAGCCCTTCAGCGCTCGTGTCTGCTCTATGTGAT 131
QY 1022 TGCATGCCACGTTGCCAGGCACTTTCATGCTGCTGCTCATCTTTTGGCCCTTCCTCAT 1081
DB 132 TTAACCTCCATCTTCCAGGCTGCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 190
QY 1082 GCTGGCTCAAGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTTACCGGGA 1141
DB 191 GCTGGCTCAAGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTTAAAGGAT 250
QY 1142 GGTGGAACCTCAAGCTCTTCTTCCAACTACTACCGACCTTGAAGCTGCTGCTGCTGCTG 1201
DB 251 GGTGGAACCTCCAGCTCATCTTCCAACTATATAGAACCTGGAATCTGCTGCTGCTGCTG 310
QY 1202 GCTGTACAGCTACGCTGATCAGGATGGCTGCGGCTCTTGGTCCCGGCGCGAGGG 1261
DB 311 GGCTATATTTAGCTGTCTTTGCTGTCTGCTGTAGTACAGCAATATGCTTGGCTGTTT 370
QY 1262 TAGCCATGCTGGGTGTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
DB 371 CTGCCATGTTAGCTGTCTTTGCTGTCTGCTGTAGTACAGCAATATGCTTGGCTGTTT 430
QY 1322 TCCTGGGGTCTTCTATCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
DB 431 GCTTGAGCTTTTCTATCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
QY 1382 ACTTCATGATCATGACGACGCGACCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
DB 491 ACTTCATGCTCAATAGTAGTCGGAAGAGCCGATTTGAATGTTCTGTGATGGACTTCTC 550
QY 1442 TGTTCTAGCGGCAAGTCCAGGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
DB 551 TTTTCTTGGGCAATGGAGCTTACTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 610
QY 1502 ACTGCCCTTACCCCGGCAACTTTCGG 1530
DB 611 ACTGCTCTCTGAAAAAATCCCATTTTGG 639

RESULT 10
LOCUS AI049480
DEFINITION 731 bp mRNA linear EST 08-JUL-1998
ub37ell.r1 Soares_thymus_2NBMT Mus musculus cDNA clone
IMAGE:1379948 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE
(HUMAN); gb:L42293 Mus musculus acyl-coenzyme A:cholesterol
acyltransferase (MOUSE);, mRNA sequence.
ACCESSION AI049480
VERSION AI049480.1 GI:3297767
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 731)
AUTHORS Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

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Db	550	ATTCTCAAGAGTGGTATGCCGCCGAGCAGCTGTCTCTGAGAACCTCATTTCTGG	605
RESULT 11			
AU099137			
LOCUS	AU099137	300 bp	mRNA linear ; EST 05-APR-2001
DEFINITION	HEP20912 similar to Homo sapiens acyl Coenzyme A:cholesterol		
	acyltransferase 2 mRNA, mRNA sequence.		
ACCESSION	AU099137		
VERSION	AU099137.1	GI:13550266	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 300)		
AUTHORS	Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata		
	H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo		
	K., Suyama,A. and Sugano,S.		
TITLE	In silico mapping of the 5'-ends of human mRNAs using full-length		
	oligo-capping method		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yutaka Suzuki		
	Department of Virology		
	Institute of Medical Science, University of Tokyo		
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan		
	Email: yusuzuki@ims.u-tokyo.ac.jp		
	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,A.		

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FEATURES
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      /note="Differential display comparison of untreated and
      dimethylfumurate treated 037 cells"
      78 a 79 c 108 g 35 t

BASE COUNT
ORIGIN
  Query Match 15.3%; Score 240; DB 9; Length 300;
  Best Local Similarity 100.0%; Pred No. 1.1e-45;
  Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCAGCGGGCCCCGCTCTCGTCTCGAGAGGACAGAAAGGCTGGGAGGGAGCGG 60
Db 61 ATGGAGCAGCGGGGGCCGCTCTCGTCTCGAGAGGACAGAAAGGCTGGGAGGGAGCGG 120
QY 61 GAGCGCCAAACCTCTGAGATGGAAACACTGAGACGACAGAGCCCCGGACTTCGTACAA 120
Db 121 GAGCGCCAAACCTGTGAGATGGAAACACTGAGACGACAGAGCCCCGGACTTCGTACAA 180
QY 121 TGGACCCGACACATGGAGGCTGTGAAGGCACAAATTGCTGGAGCAAGCGCAGGACAACTG 180
Db 181 TGGACCCGACACATGGAGGCTGTGAAGGCACAAATTGCTGGAGCAAGCGCAGGACAACTG 240
QY 181 AGGAGCTGCTGGATCGGGCCATCGCGGAGGCTATACAACTCTACCATCACAGACAAA 240
Db 241 AGGAGCTGCTGGATCGGGCCATCGCGGAGGCTATACAACTCTACCATCACAGACAAA 300

RESULT 12
BG500675
LOCUS BG500675
DEFINITION 602547088F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669480 5',
mRNA sequence.
ACCESSION BG500675.
VERSION BG500675.1 GI:13462192
KEYWORDS EST.
SOURCE human.

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BG500675  
 LOCUS  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE



provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Patricia Bonaldo."

BASE COUNT 172 a 210 c 223 g 282 t  
ORIGIN

Query Match 14.9%; Score 233.8; DB 9; Length 887;  
Best Local Similarity 64.1%; Pred. No. 5.2e-44;  
Matches 352; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1005 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 1064  
Db 2 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 61

QY 1065 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 1124  
Db 62 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 121

QY 1125 GATGTTCTACCGGAGTGTGGAACTCAAGCTTCTCCAACTACTACCGACTTGGAA 1184  
Db 122 GATGTTCTACCGGAGTGTGGAACTCAAGCTTCTCCAACTACTACCGACTTGGAA 181

QY 1185 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 1244  
Db 182 CTTGGTCTCTATCTGATGCGAGTTCGAGCATCTTCATGCTGCTCATCTT 241

QY 1245 TGGCCGGGCGGAGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1304  
Db 242 GAAGAGTTCAAACTTCCGCGCATGCTGGAGCTTCTGCGCTGCTGCTGCTGCT 301

QY 1305 GTATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1364  
Db 302 GTATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

QY 1365 CATTGGAGGAATCTGAACCTTCAATGATGATGATGATGATGATGATGATGATGAT 1424  
Db 362 CATTGGAGGAATCTGAACCTTCAATGATGATGATGATGATGATGATGATGATGAT 421

QY 1425 GCTGATGTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1484  
Db 422 CATGGTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481

QY 1485 GTGTAGCGACGGCGGAGTCCCTTACCCAGGCACTTCTGGGGCTGGTGCAC 1544  
Db 482 GTGTAGCGACGGCGGAGTCCCTTACCCAGGCACTTCTGGGGCTGGTGCAC 541

QY 1545 TCGATCTTG 1553  
Db 542 GCGACCTGG 550

RESULT 14  
AG133295  
LOCUS 635 bp DNA linear GSS 04-NOV-2001  
DEFINITION Pan troglodytes DNA, clone: PTB-145020.F, genomic survey sequence.  
ACCESSION AG133295  
VERSION AG133295.1 GI:16662973  
KEYWORDS GSS.  
SOURCE Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male BAC Library clone:PTB-145020.F.

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.  
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library PTB  
Unpublished

2 (bases 1 to 635)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

## COMMENT

and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shimocho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: shimbos@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKSL45  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 635  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-145020.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
BASE COUNT 103 a 217 c 189 g 126 t  
ORIGIN

Query Match 14.5%; Score 227.6; DB 17; Length 635;

Best Local Similarity 90.6%; Pred. No. 1.3e-42;  
Matches 259; Conservative 0; Mismatches 14; Indels 13; Gaps 1;

QY 442 AGGCTGCTCTGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCATTGGCGT 501  
Db 147 AGGCTGCTCTGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCATTGGCGT 206

QY 502 GTGACCTGGTGGTCCCATGTTCTGTCCACCTGTTGGCGCCGTACAGCCCTACGGT 561  
Db 207 GTGACCTGGTGGTCCCATGTTCTGTCCACCTGTTGGCGCCGTACAGCCCTACGGT 266

QY 562 TGGGCGAG-----GGGACCTGTGAGCAGGAGCGCGCTGGCTGTGCGCT 508  
Db 267 TGGGCGAG-----GGGACCTGTGAGCAGGAGCGCGCTGGCTGTGCGCT 326

QY 609 TTATAGCGCCAGCGCGTGTGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCT 568  
Db 327 GCTAGCGCCAGCGCGTGTGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCTGTGCGCT 386

QY 669 GCTCCGCGCGCGCTCCCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 714  
Db 387 GCTCCGCGCGCGCTCCCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 432

## RESULT 15

BG697784

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG697784 848 bp mRNA linear EST 07-MAY-2001  
602661272F1 NC1\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4804481 5',  
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 848)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:

source

BASE COUNT  
ORIGIN

<b>Matches</b>	<b>340;</b>	<b>Conservative</b>	<b>0;</b>	<b>Mismatches</b>	<b>196;</b>	<b>Indels</b>	<b>0;</b>	<b>Gaps</b>	<b>0;</b>
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Db 4 CCATCTTGCCAGGTGTGCTGATTCTCTTCCCTTACTTTTGGCCTTTTGGCACTGCTGGC 63

QY 1V88 ICAACGCCCTTGGCCGAGATGCTACGATTTGGAGACAGGATGTCTACCGGGACTGGTGGATT

DB 64 TCAATGCCCTTTGCTGAGATGTTACGCTTTGGTGACAGGATGTTCTATAGAAGGATTTGGTGA 123

QY 1148 ACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATGACTGGCTGT 1207

D<sub>b</sub> 124 ACTCCACGTCATACTCCAACTATTATAGAACCTGGAAATGTGGTGGTCCATGACTGGCTAT 183

1208 ACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGCCGAGGGTAGCCA 1267

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Db 424 TGGGCAATGGAGTCTTACTCTGCTTTTATTCTCAAGAAATGGTATGCACGTACGACTGC 483

QY 1508 CCTTACCCAGGCAACTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT 1563

Db 484 CTCTGAAAAATCCCACATTTTGGATTATGTCCGGCCACGTTCTCTGGACCTTGTCGT 539

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